Immediate

CTL activ CTL activ HV gp120 Bpendymin Peptide T AIDS viru Peptide T HV.1 gp1 HV.3 gp2 Sequence env prote ARV-2 env AIV-1 (AT AINS asso ARV-2 env HIV-1 (AT AINS asso ARV-2 env HIV-1 (AT AINS asso ARV-2 env HIV-1 (AT AINS asso

Aab99509
Abr62030
Abr62033
Adn14264
Adw05584
Aax 98995
Aar7826
Abp52855
Aam5231
Aar290181
Aar290181
Aar29711
Aar29718

AAB99509
ABR62037
ABR62037
ABR62037
AAN05284
AAN05284
AAR71264
AAR771264
AAR7726
ABP52855
AAR7726
ABP52855
AAR23311
AAR23311
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AAR35787

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Aapp33007 Blocking
Aapp1832 Octapepti
Aapp1832 Octapepti
Aar13201 Sialic ac
Aar26900 Herpes si
Aar2833 Peptide T
Aar44334 Peptide T
Aar44342 Peptide T
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Aar59486 Prototype
Aar59489 Peptide T
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Aar59480 Peptide T
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Aar51480 Peptide T
Aar61480 Peptide T
Aar61481 Prototype
Aav45929 Complex g
Aav45934 HIV gpl20
Aav36931 Nortus rel
Aab52347 Virus rel
Aab52331 Virus rel
Aab52331 Virus rel
                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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      GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                          2105692 segs, 386760381 residues
                                                                                                                                                                                                                                                                                                                                               SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                     OM protein - protein search, using sw model
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AAP91880
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RESULT.1  MAPP31007 standard; protein; 8 AA.  AC AAP831007;  XZ  AAP831007;  XX  AAP831007;  XX  Blocking peptide used in composition for treatment and diagnosis of HIV (pp.10; monoclonal antibodies; neutralising region.  XX  HIV; gpl10; monoclonal antibodies; neutralising region.  XX  MIV; gpl10; monoclonal antibodies; neutralising region.  XX  MAX-1986; 86U3-00898273.  PR 01-MAY-1986; 86U3-00898273.  PR 19-AUG-1986; 86U3-00898273.  PR 10-MAY-1997; 87U3-00065026.  PR 10-MAY-1997; 87U3-00065026.  PR 10-MAY-1997; 87U3-00065026.  PR 20-MU-1987; 87U3-00065026.  PR 10-MAY-1997; 87U3-00065026.  PR 20-UM-1987; 87U3-0005701.  A (GENE-) GENETIC SYSTEMS CORP.  XX  XX  XX  XX  XX  XX  XX  XX  XX		ALIGNMENTS	
AAPB3007; 25-MAR-2003 (revised) 10-DEC-1990 (first entry) Blocking peptide used in composition for treatment and diagnosis infections. HIV; gpl10; monoclonal antibodies; neutralising region. HOMO sapiens. GB2196634-A. 05-MAY-1988. 19-AUG-1986; 86US-00898273. 01-MAY-1988. 19-AUG-1986; 86US-00898273. 01-MAY-1987; 87US-00045026. 07-OCT-1987; 87US-00067996. 07-OCT-1987; 87US-00067996. 07-OCT-1987; 87US-00105761. GGENE-) GENETIC SYSTEMS CORP. Shriver MK; WPI; 1988-103268/15. Monoclonal antibodies and peptide(s) - useful for treatment and of human immuno:deficiency virus infections. Claim 41; Page 24; 25pp; Bnglish. A blocking peptide contg. at least 5 adjacent amino acids from typullo envelope glycoprotein sequence inhibits virus prolif- erating useful, in conjunction with a monoclonal antibody to a neutral region of HIV, for treatment or prophylaxis of HIV infections. Reminals can have up to 20 amino acids attended. See also AAPB3 and AAPB3108-12. This is equivalent to NLG701950 (accession not this). (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct DR Sequence 8 AA;	RESU AAP8 ID	SULT 1 P83007 AAP83007 standard; protein; 8	
25-MAR-2003 (revised) 10-DEC-1990 (first entry) Blocking peptide used in composition for treatment and diagnosis infections. HIV; gpl10; monoclonal antibodies; neutralising region. Homo sapiens. GB2196634-A. 05-MAY-1988; 87GB-00019587. 20-AUG-1986; 86US-000898273. 01-AUG-1987; 87US-00067926. 02-AUG-1987; 87US-00067926. 03-AUN-1987; 87US-00067926. 03-UNN-1987; 87US-00067926. 04-AUG-1988; 86US-00067926. 05-MAY-1989; 87US-00067926. 07-OCT-1989; 87US-00067926. 07-OCT-1989; 87US-00067996. 07-OCT-1980; 87US-0007696; 97US-0007696. 07-OCT-1980; 97US-0007696; 97US-	X S		
Blocking peptide used in composition for treatment and diagnosis infections.  HIV; gpl10; monoclonal antibodies; neutralising region.  Homo sapiens.  GB2196634-A.  05-MAY-1988.  19-AUG-1987; 87GB-00019587.  20-MAY-1987; 87US-00045026.  20-JUN-1987; 87US-00067996.  07-OCT-1987; 87US-00067996.  07-OCT-1987; 87US-00067996.  07-OCT-1987; 87US-00067996.  07-OCT-1987; 87US-00067996.  07-OCT-1987; 87US-00067996.  07-OCT-1987; 87US-00105761.  (GENE-) GENETIC SYSTEMS CORP.  Shriver MK;  WPI; 1988-103268/15.  Monoclonal antibodies and peptide(s) - useful for treatment and of human immuno:deficiency virus infections.  Claim 41; Page 24; 25pp; Bnglish.  A blocking peptide contg. at least 5 adjacent amino acids from tapilo envelope glycoprotein sequence inhibite virus prolife-erating useful, in conjunction with a monoclonal antibody to a neutral engion of HIV, for treatment or prophylaxis of HIV infections. Netwinals can have up to 20 amino acids attached. See also AAPB and AAPB3008-12. This is equivalent to NL8701950 (accession notthis). (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct DR Sequence 8 AA;	<b>3</b> 55	25-MAR-2003 10-DEC-1990	
HIV; gpl10; monoclonal antibodies; neutralising region.  Homo sapiens.  GB2196634-A.  05-MAY-1988.  19-AUG-1987; 87GB-00019587.  20-AUG-1986; 86US-00898273.  01-MAY-1987; 87US-00045026.  29-UUN-1987; 87US-00105761.  GENE-) GENETIC SYSTEMS CORP.  Shriver MK;  WPI; 1988-103268/15.  Monoclonal antibodies and peptide(s) - useful for treatment and of human immuno:deficiency virus infections.  Claim 41; Page 24; 25pp; Bnglish.  A blocking peptide contg. at least 5 adjacent amino acids from to gpl10 envelope glycoprotein sequence inhibits virus prolif-eratis useful, in conjunction with a monoclonal antibody to a neutral subsetul, in conjunction with a monoclonal antibody to a neutral subsetul, in conjunction with a monoclonal antibody to a neutral subsetul, in conjunction with a monoclonal antibody to a neutral subsetul, in conjunction with a monoclonal antibody to a neutral subsetul, in conjunction with a monoclonal antibody to a neutral subsetul, in conjunction with a monoclonal antibody to a neutral subsetul, in conjunction with a monoclonal antibody to a neutral subsetul, in conjunction with a monoclonal antibody to a neutral subsetul, in conjunction with a monoclonal antibody to a neutral subsetul, in conjunction with a monoclonal antibody to a neutral subsetul, in conjunction with a monoclonal antibody to a neutral subsetul, in conjunction with a monoclonal antibody to a neutral subsetul, in conjunction with a monoclonal antibody to a neutral subsetul, in conjunction with a monoclonal antibody to a neutral subsetul, in conjunction with a monoclonal antibody to a neutral subsetul, in conjunction with a monoclonal antibody to a neutral subsetul, in conjunction with a monoclonal antibody to a neutral subsetul, in conjunction with a monoclonal antibody to a neutral subsetul, in conjunction with a monoclonal antibody with a monoclo	X E E S	Blocking peptide used in infections.	and diagnosis
Homo sapiens.  GB2196634-A.  05-MAY-1988.  19-AUG-1987; 87GB-00019587.  20-AUG-1987; 87US-00045026.  29-UNN-1987; 87US-00067996.  01-MAY-1987; 87US-00105761.  (GENE-) GENETIC SYSTEMS CORP.  Shriver MK;  WPI; 1988-103268/15.  Monoclonal antibodies and peptide(8) - useful for treatment and of human immuno:deficiency virus infections.  Claim 41; Page 24; 25pp; Bnglish.  A blocking peptide contg. at least 5 adjacent amino acids from to gpilo envelope glycoprotein sequence inhibits virus prolif-eratis useful, in conjunction with a monoclonal antibody to a neutra region of HIV, for treatment or prophylaxis of HIV infections. Netwinals can have up to 20 maino acids attached. See also AAPR3 and AAPR3108-12. This is equivalent to NuB701950 (accession no. this). (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct DR Sequence 8 AA;	₹ } ;	HIV; gp110; monoclonal	
GB2196634-A.  05-WAY-1988.  19-AUG-1987; 87GB-00019587.  20-AUG-1986; 86US-00898273.  01-WAY-1987; 87US-00045026.  29-UNN-1987; 87US-00105761.  (GENE-) GENETIC SYSTEMS CORP.  Shriver MK;  WPI; 1988-103268/15.  Monoclonal antibodies and peptide(s) - useful for treatment and of human immuno:deficiency virus infections.  Claim 41; Page 24; 25pp; Bnglish.  A blocking peptide contg. at least 5 adjacent amino acids from tegino of HIV, for treatment to nprophylaxis of HIV infections.  A blocking peptide contg. at least 5 adjacent amino acids from tegino of HIV, for treatment or prophylaxis of HIV infections. Neghio envelope glycoprotein sequence inhibits virus prolif-eratis useful, in conjunction with a monoclonal antibody to a neutra region of HIV, for treatment or prophylaxis of HIV infections. Netwinals can have up to 20 amino acids attached. See also AAPR3 and AAP831008-12. This is equivalent to NLB701950 (accession no. this). (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct DR Sequence 8 AA)	ខ្ល		
05-MAY-1988.  19-AUG-1987; 87GB-00019587.  20-AUG-1986; 86US-000898273. 01-MAY-1987; 87US-0005796. 29-UUN-1987; 87US-00105761. (GENE-) GENETIC SYSTEMS CORP. Shriver MK; WPI; 1988-103268/15.  Monoclonal antibodies and peptide(s) - useful for treatment and of human immuno:deficiency virus infections.  Claim 41; Page 24; 25pp; Bnglish. A blocking peptide contg. at least 5 adjacent amino acids from tregion of HIV, for treatment or prophylaxis of HIV infections. A blocking peptide contg. at least 5 adjacent amino acids from tregion of HIV, for treatment or prophylaxis of HIV infections. N terminals can have up to 20 mmino acids attached. See also AAPB3 and AAPB3008-12. This is equivalent to NUB701950 (accession no. this). (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct DR Sequence B AA;	X Z		
19-AUG-1987; 87GB-00019587.  20-AUG-1986; 86US-00089273. 01-MAY-1987; 87US-00045026. 29-JUN-1987; 87US-00165761. (GENE-) GENETIC SYSTEMS CORP. Shriver MK; WPI; 1988-103268/15. Monoclonal antibodies and peptide(s) - useful for treatment and of human immuno:deficiency virus infections.  Claim 41; Page 24; 25pp; Bnglish. A blocking peptide contg. at least 5 adjacent amino acids from tregion of HIV, for treatment or prophylaxis of HIV infections. A blocking peptide contg. at least 5 adjacent amino acids from tregion of HIV, for treatment or prophylaxis of HIV infections. N terminals can have up to 20 maino acids attached. See also AAP83 and AAP83008-12. This is equivalent to NUB701950 (accession no. this). (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct DR Sequence 8 AA;	<b>설립</b>		
20-AUG-1986; 86US-00898273. 01-MAY-1987; 87US-00067996. 29-UUN-1987; 87US-00067996. 07-OCT-1987; 87US-00105761. (GENE-) GENETIC SYSTEMS CORP. Shriver MK; WPI; 1988-103268/15. Monoclonal antibodies and peptide(s) - useful for treatment and of human immuno:deficiency virus infections. Claim 41; Page 24; 25pp; English. A blocking peptide contg. at least 5 adjacent amino acids from t gpl10 envelope glycoprotein sequence inhibits virus prolif- eratis useful, in conjunction with a monoclonal antibody to a neutra region of HIV, for treatment or prophylaxis of HIV infections. Neterninals can have up to 20 amino acids attached. See also AARB3 and AAP83008-12. This is equivalent to NLB701950 (accession no. this). (Updated on 25-MAR-2003 to correct DR Sequence 8 AA;	X E	19-AUG-1987;	
01-MAY-1987; 870S-00067996. 07-OCT-1987; 870S-00105761. (GENE-) GENETIC SYSTEMS CORP. Shriver MK; WPI; 1988-103268/15. Monoclonal antibodies and peptide(s) - useful for treatment and of human immuno:deficiency virus infections. Claim 41; Page 24; 25pp; Bnglish. A blocking peptide contg. at least 5 adjacent amino acids from tregion of HIV, for treatment or prophylaxis of HIV infections. N terminals can have up to 20 amino acids attached. See also AAP83 and AAP83008-12. This is equivalent to NUB701950 (accession no. this). (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct DR Sequence B AA;	X & :	20-AUG-1986;	
GENE-) GENETIC SYSTEMS CORP.  Shriver MK;  WPI; 1988-103268/15.  Monoclonal antibodies and peptide(s) - useful for treatment and of human immuno:deficiency virus infections.  Claim 41; Page 24; 25pp; English.  A blocking peptide contg. at least 5 adjacent amino acids from tregion of HIV, for treatment or prophylaxis of HIV infections. N terminals can have up to 20 amino acids attached. See also AAPB3 and AAPB3008-12. This is equivalent to NUB701950 (accession no. this). (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct DR Sequence B AA;	¥	01-MAY-1987; 29-JUN-1987;	
(GENE-) GENETIC SYSTEMS CORP.  Shriver MK;  WPI; 1988-103268/15.  Monoclonal antibodies and peptide(s) - useful for treatment and of human immuno:deficiency virus infections.  Claim 41; Page 24; 25pp; Bnglish.  A blocking peptide contg. at least 5 adjacent amino acids from tregion envelope glycoprotein sequence inhibits virus prolif-eratis useful, in conjunction with a monoclonal antibody to a neutra region of HIV, for treatment or prophylaxis of HIV infections. Netrminals can have up to 20 mmino acids attached. See also AAPB3 and AAPB3008-12. This is equivalent to NUB701950 (accession no. this). (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct DR Sequence 8 AA);	% %	07-OCT-1987;	
Shriver MK; WPI; 1988-103268/15.  Monoclonal antibodies and peptide(s) - useful for treatment and of human immuno:deficiency virus infections.  Claim 41; Page 24; 25pp; English.  A blocking peptide contg. at least 5 adjacent amino acids from tgp110 envelope glycoprotein sequence inhibits virus prolif-eratis useful, in conjunction with a monoclonal antibody to a neutra region of FIIV, for treatment or prophylaxis of HIV infections. Nerminals can have up to 20 amino acids attached. See also AAR81 and AAP83008-12. This is equivalent to NL9701950 (accession no. this). (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct DR Sequence 8 AA;	\$ <b>&amp;</b> \$	(GENE-) GENETIC SYSTEMS	
WPI; 1988-103268/15.  Monoclonal antibodies and peptide(s) - useful for treatment and of human immuno:deficiency virus infections.  Claim 41; Page 24; 25pp; English.  A blocking peptide contg. at least 5 adjacent amino acids from tgpl10 envelope glycoprotein sequence inhibits virus prolif-eratis useful, in conjunction with a monoclonal antibody to a neutra region of HIV, for treatment or prophylaxis of HIV infections. Nerminals can have up to 20 amino acids attached. See also AAPB3 and AAPB3008-12. This is equivalent to NLB701950 (accession no. this). (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct DR Sequence 8 AA;	됩		
Monoclonal antibodies and peptide(s) - useful for treatment and of human immuno:deficiency virus infections.  Claim 41; Page 24; 25pp; Bnglish.  A blocking peptide contg. at least 5 adjacent amino acids from tregion envelope glycoprotein sequence inhibits virus prolif-eratis useful, in conjunction with a monoclonal antibody to a neutra region of HIV, for treatment or prophylaxis of HIV infections. Netrminals can have up to 20 amino acids attached. See also AAPB3 and AAPB3008-12. This is equivalent to NuB701950 (accession no. this). (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct DR Sequence 8 AA;	X E		
Claim 41; Page 24; 25pp; English.  A blocking peptide contg. at least 5 adjacent amino acids from th gpl10 envelope glycoprotein sequence inhibits virus prolifeeratis useful, in conjunction with a monoclonal antibody to a neutral region of HIV, for treatment or prophylaxis of HIV infections. Neterinals can have up to 20 amino acids attached. See also AAPPB30 and AAPB3008-12. This is equivalent to NLB701950 (accession no. 1 this). (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct DR Sequence 8 AA;	\$ <b>t</b> t t	Monoclonal antibodies and peptide(s) - of human immuno:deficiency virus infect	ul for treatment .
A blocking peptide contg. at least 5 adjacent amino acids from the gpl10 envelope glycoprotein sequence inhibits virus prolif-eratis useful, in conjunction with a monoclonal antibody to a neutral region of HIV, for treatment or prophylaxis of HIV infections. Neterminals can have up to 20 amino acids attached. See also AAPB30 and AAPB3008-12. This is equivalent to NL8701950 (accession no. ithis). (Updated on 25-MAR-2003 to correct PF field.) (Updated on 2003 to correct PR field.) Sequence 8 AA;	X S S	Claim 41; Page 24; 25pp;	
gpli0 envelope glycoprotein sequence inflibits virus prolif- eratil is useful, in conjunction with a monoclonal antibody to a neutral region of HIV, for treatment or prophylaxis of HIV infections. N-terminals can have up to 20 amino acids attached. See also AAP830 and AAP83008-12. This is equivalent to NL8701950 (accession no. ithis). (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct DR Sequence 8 AA;	ខម	A blocking peptide contg. at least 5	
region of HIV, for treatment or prophylaxis of HIV infections. N- terminals can have up to 20 amino acids attached. See also AAPP830 and AAPB3008-12. This is equivalent to NLB701950 (accession ADP. 31 this). (Updated on 25-MAR-2003 to correct PF field.) (Updated on 2003 to correct PR field.) (Updated on 25-MAR-2003 to correct DR Sequence 8 AA;	88		orolli- eration. I to a neutralising
and AAPB3008-12. This is equivalent to NL8701950 (accession no. i this). (Updated on 25-MAR-2003 to correct PF field.) (Updated on 2003 to correct PR field.) (Updated on 25-MAR-2003 to correct DR Sequence 8 AA;	ខ្ល	region of HIV, for tre terminals can have up	of HIV inf sched. See
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cell surface receptor (CD4) binding. CD4 slite is common to the CNS and favourably to treatment with the peptide-containing composition. There are a range of forms which the composition and administration can take. The aminor-terminal Alanine is D-Ala. (Note: Revised entry submitted to correct the patent number format of US Government-owned NTIS applications to prevent clashes with ongoing US granted patent numbers. For further www.derwent.com/dwpi/updates/niis us.html.) (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PF field.)
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                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     Use of short peptide(s) to inhibit binding of HIV to human cells - treating psoriasis and neuro:psychiatric disorder including memory deficiency and mood disorder.
                                                                                                                                                                                                     Octapeptide which inhibits HIV binding to cell surface receptors.
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       100.0%; Score 41; DB 1; Length 8; 100.0%; Pred. No. 1.8e+06;
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                           Mismatches
                                                                                                                                                                                                                          HIV; psoriasis; neuropsychiatric disorders
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                                                                                                                  AAP91830 standard; peptide; 8 AA.
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88US-00285559
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17-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of short peptide(s) to inhibit binding of HIV to human cells - for treating psoriasis and neuro:psychiatric disorder including memory deficiency and mood disorder.
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                                                                                                                                                                                                            Octapeptide which inhibits HIV binding to cell surface receptors.
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100.0%; Pred. No. 1.8e+06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                  HIV; psoriasis; neuropsychiatric disorders.
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(USDC ) US SEC OF COMMERCE.
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AAP91832 standard; protein; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89US-00352313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88US-00199873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88US-00285559
                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                               (revised)
(revised)
(revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003 (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bridge P, Goodwin FK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1989-378088/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASTITINY 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ASTITINYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-MAY-1989;
                                                                                                                                                                                                                                                                                                                         Inidentified
                                                                                                                                                                                                                                                                                                                                                                       USN7352313-N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-MAY-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-DEC-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                        10-OCT-1989.
                                                                                                                                                                     22-MAY-1990
                                                                                                    25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR13201;
                                                   AAP91832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR13201
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Gaps

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Indels

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The peptide is useful in the treatment and prevention of diseases or conditions caused by Herpes viruses, esp. Herpes Simplex Virus-1 (HSV-1), Hugh (VEV), Muran cytomegalovirus (HTV) or Epstein-Barr Virus (EBV). It can also be used to treat diseases and conditions caused by the family of herpes viruses in animals, e.g. Aljeazky's disease in pigs, bovine rhinocrachettis, rhinopharyrgitis in houters, laryngotracheitis in poultry for herpes viruses in animals, e.g. Aljeazky and also be used in diagnostics. The peptide has never been reported to penetrate any type of cells, but only to occupy the CD4 receptors found on 1 ymphocytes and it apparently penetrates the skin with relative ease. A major advantage of the peptide is its almost complete lack of toxicity, which means that the use of high doses for an extended period of time is peptide (ARR26905,6). See also ARR269011826906. (Updated on 25-MAR-2003) to correct PF field.)
                                                                                                                                                                                                                                        New linear or cyclic peptide(s) including cysteine residue - occupy lymphocyte CD4 receptors, for treating and preventing virus infections with Herpes simplex, Varicella zoster, cytomegalovirus and Epstein-Barr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Revised record issued on 23-SEP-2004 : Correction to Feature Table Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CFS; fatigue; tension; anger; confusion; peptide T; HIV; synthetic; human immunodeficiency virus; gp 120; protein kinase A; enhancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 41; DB 2; Length 100.0%; Pred. No. 1.8e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "may be amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Ala, D-Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR28939 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                 Claim 5; Page 15; 21pp; English.
                                                                                              91DK-00000319
                                                                                                                              (CARL-) CARLBIOTECH LTD AS.
                                                                                                                                                                    Pedersen O, Macfadden DK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
                                                                                                                                                                                                      WPI; 1992-316120/38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ASTTTNYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CFS; fatigue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9219257-A1
                      03-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
23-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR28939;
                                                                                                                                                                                                                                                                                                   virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The prod. has prolonged half-life and is used as a pharmaceutical for treatment of various diseases, such as cataract and immune disorders. It comprises a peptide, N-terminally glycosylated by (opt. acetylated) sialic acid. See also AAR12932, AAR13162 and AAR13201. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New sialic acid derivs. bonded to physiologically active polypeptide -
for treatment of cataracts, immune disorders etc. with prolonged half-
                                                                                                                                                                                 /note= "N-terminally glycosylated by 5-acetamido-
2,4,7,8,9-penta-O-acetyl-3,5-deoxy-beta- D-glycero-D-
galactononulopyranosonyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSV; HSV-1; HSV-2; Varicella Zoster virus; human cytomegalovirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 41; DB 2; Length 8; 100.0%; Pred. No. 1.8e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Herpes simplex virus treatment peptide.
                                                                       Sialic acid; cataract; immune disorder.
                                   Sialic acid-bonded polypeptide (3).
                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 5; Page 6; 7pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR26900 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Thr-NH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= D-Ala
                                                                                                                                                                                                                                                                                                                                 89JP-00288560,
                                                                                                                                                                                                                                                                                                                                                                 89JP-00288560
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(revised)
(first entry)
10-OCT-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1991-233839/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ASTITINY 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                     (MECT-) MECT CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ASTTTNYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8 AA;
                                                                                                                                             Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                         JP03151398-A
                                                                                                                                                                                                                                                                                                                             06-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                   06-NOV-1989;
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20-MAY-1998
                                                                                                           Synthetic
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AAR26900

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Gaps

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93WO-GB000649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-MAR-1993;
                           Andersen AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9320102-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-OCT-1993
                                                                                                                                                                                                                                                                                                                             8;
                                    Phipps DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR44334;
(PEPT-)
(DRUG-)
                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                     AAR44334
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                                                                                                                                                       Peptide T is a protein kinase A enhancer which produces both symptomatic and functional improvement in patients with chronic fatigue syndrome, and bas a sequence derived from a sub region of HIV gpl20 responsible for binding to brain membrane and human T cells. The sequence may be used to design a synthetic peptide which may be used for treatment of chronic fatigue syndrome not associated with HIV infection. The peptide will reduce fatigue, tension, anger and confusion and improves cognitive and neuromoter performance. See also AAR28918-42. (Updated on 25-WAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "one or more of these sites can be glycosylated"
                                                                                                            Peptide compans, for treating chronic fatigue syndrome - ameliorate symptoms and improve vigour and cognitive and neuro-motor performance.
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inflammation; antiinflammatory; immunomodulator; HTLV-1; multiple sclerosis; myopathy; chronic fatigue syndrome; toxic shock; arthritis; inflammatory bowel disease; host-versus-graft; graft-versus-host; transplant.
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0
                                                                                                                                                                                                                                                                        Length 8;
                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide T related peptide for treating inflammation.
                                                                                                                                                                                                                                                                        Score 41; DB 2; I
Pred. No. 1.8e+06;
                                                                                                                                                                                                                                                                                         0; Mismatches
                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                         Disclosure, Page 18, 21pp, English.
                                                                                                                                                                                                                                                                                                                                                                            AAR44336 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "D-Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92DK-00000645.
92US-00915118.
92US-00987674.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93WO-GB000649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92US-00858832
                   92WO-US003582
                                     91US-00696556
                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 8; Conservative
                                                                          Goodwin FK;
                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
                                                                                                                                                                                                                                                                                                             œ
                                                                                            WPI; 1992-398525/48
                                                                                                                                                                                                                                    correct PN field.)
                                                                                                                                                                                                                                                                                                             1 ASTITINYI
                                                                                                                                                                                                                                                                                                                               ASTTTNYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                      Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Modified-site
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17-JUL-1992;
09-DEC-1992;
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                    08-MAY-1992;
                                      08-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
22-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9320102-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-OCT-1993.
                                                                           Bridge TP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                               AAR44336;
                                                                                                                                                                                                                                                                                                                                                          RESULT 7
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The invention relates to a group of linear or cyclic tetra- to decate peptides which include Peptide T and its analogues, where at least one of the amino acids may optionally have a monomeric or polymeric carbohydrate substituted onto a hydroxyl, amino and/or amido group. In one aspect the invention relates to the use of these peptides for the treatment of invention and in another aspect it relates to those peptides in which the carbohydrate moiety is present (other than glycosylated Prototype Peptide T) as new chemical entities. The present peptide is one of 10 specific peptides listed in a sub-claim for use in the treatment of inflammation. The peptides as immunomodulators in the treatment and prevention of inflammation. In particular they can be used in the treatment of multiple sclerosis, myopathies (including HTLV-1 associated myopathies) and symptoms and diseases associated with chronic immune activation including chronic fatigue syndrome, toxic shock, arthritis, inflammatory bowel disease, and host-versus-fraft and graft-versus-host responses in transplant recipients. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                           New linear and cyclic peptide T analogues - used for treatment and prevention of inflammation, e.g. multiple sclerosis and myelopathies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inflammation; antiinflammatory; immunomodulator; HTLV-1; multiple sclerosis; myopathy; chronic fatigue syndrome; toxic shock; arthritis; inflammatory bowel disease; host-versus-graft;

    .8
/note= "one or more residues may be glycosylated"

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                                                                                                       Macfadden DK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide T related peptide for treating inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 41; DB 2; L
100.0%; Pred. No. 1.8e+06;
iive 0; Mismatches 0;
                                                                                                           Doob PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                       PL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR44334 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Page 83; 103pp; English.
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                                                                                                           Carlen
Widmer
PEPTIDE TECHNOLOGY LTD. DRUG ROYALTY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "D-Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             graft-versus-host; transplant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                       ', Aston R,
Rathjen D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
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Best Local Similarity
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Macfadden DK;

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The invention relates to a group of linear or cyclic tetra- to decapeptides which include Peptide T and its analogues, where at least one of the amino acids may optionally have a monomeric or polymeric carbohydrate substituted onto a hydroxyl, amino and/or amido group. In one aspect the invention relates to the use of these peptides for the treatment of inflammation, and in another aspect it relates to those peptides in which the carbohydrate moiety is present (other than glycosylated Prototype Peptide T) as new chemical entities. The present peptide is one of 10 specific peptides listed in a sub-claim for use in the treatment of inflammation. The peptides as immunomodulators in the treatment and prevention of inflammation. In particular they can be used in the treatment of multiple sclerosis, myopathies (including HTLV-1 associated treatment of multiple sclerosis, myopathies (including HTLV-1 associated cativation including chronic fatigue syndrome, toxic shock, arthritis, inflammatory bowel disease, and host-versus-graft and graft-versus-host responses in transplant recipients. (Updated on 25-MAR-2003 to correct PN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New linear and cyclic peptide T analogues - used for treatment and prevention of inflammation, e.g. multiple sclerosis and myelopathies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inflammation; antiinflammatory; immunomodulator; HTLV-1; multiple sclerosis; myopathy; chronic fatigue syndrome; toxic shock; arthritis; inflammatory bowel disease; host-versus-graft; graft-versus-host; transplant.
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100.0%; Pred. No. 1.8e+06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                        Doob PR,
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                                                                                                                                                                                                                                                                                                                                                                                        Carlen PL,
Widmer F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Page 83; 103pp; English.
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                                                                                                                             92DK-0000645.
92US-00915118.
92US-00987674.
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                                 93WO-GB000649
                                                                                                   92US-00858832
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(first entry)
                                                                                                                                                                                                                                                                                                                  DRUG ROYALTY CORP
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Rathjen D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1993-336832/42.
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Best Local Similarity
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                                 29-MAR-1993;
                                                                                                                                    14-MAY-1992;
17-JUL-1992;
                                                                                                   27-MAR-1992
                                                                                                                                                                                                       09-DEC-1992;
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22-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                             Phipps DJ,
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                                                                                                                                                                                                                                                                                                                  (DRUG-)
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THE LEAK OX MARKAN DIX AND THE LEAK OX AND THE LEAK OX MARKAN DIX AND THE LEAK OX AND THE LEAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a group of linear or cyclic tetra- to decapeptides which include Peptide T and its analogues, where at least one of the amino acids may optionally have a monomeric or polymeric carbohydrate substituted onto a hydroxyl, amino and/or amido group. In one aspect the inflammation, and in another aspect it relates to these peptides in which the carbohydrate moiety is present (chter than glycosylated Prototype Peptide T) as one of 10 specific peptides listed in a sub-claim for use in the treatment of inflammation. The peptides act as immunomodulators in the treatment and prevention of inflammation. In particular they can be used in the treatment of multiple sclerosis, myopathies (including HTAV-1 associated myopathies) and symptoms and diseases associated with chronic immune activation including chronic fatigue syndrome, toxic shock, asthericals, inflammation; the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New linear and cyclic peptide T analogues - used for treatment and prevention of inflammation, e.g. multiple sclerosis and myelopathies.
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                                                                                                                                                                                                                                                                                                                  Macfadden DK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                           Carlen Widmer
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                         92US-00858832.
92DK-00000645.
92US-00915118.
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                                                                                                                                                                                                                                                                                                              Andersen AJ, Aston R,
Phipps DJ, Rathjen D,
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to correct PN field.
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                                                                                                                                                                                                                                                                                                           Andersen AJ,
                                                                                                                                    09-DEC-1992;
                         27-MAR-1992;
14-MAY-1992;
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                                                                                            17-JUL-1992;
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22-JUN-1994
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(DRUG-)
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Matches

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AAR44335

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The peptide, a peptide T analogue, has a high threonine content. The peptide binds to T4 receptors and is useful for intranasal admin. to prevent viral infectivity in mammals by viruses which bind to the T4 receptors. The peptide is believed to act as a competitive blocking agent. It inhibits binding of HIV gp 120 to brain tissue and inhibits HIV replication in cell culture. It can be used to alleviate the symptoms of AIDS. It can also be used to treat TSP, resulting in loss of paralysis and improvement in bladder and sexual function and decreased deterioration of memory and attention. The peptide may also be used in vaccines to prevent the transmission of HIV. See also AAR47826-39. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                           Compsns. to treat tropical spastic paresis and immunodeficiency - contain peptide to block receptor binding or viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide T; prototype; octapeptide; eczema; dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 41; DB 2; I
100.0%; Pred. No. 1.8e+06;
                                                                                                                                                                                                    (ADPE-) ADVANCED PEPTIDES & BIOTECHNOLOGY SCI.
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                                                                                                                                                                                                                                                                                                                                                                          Claim 6; Page 16; 22pp; English.
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26-NOV-1995 (first en
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                                                                                                                             20-MAY-1993;
                                                                                                                                                                  L5-JUN-1992;
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                                                    EP579363-A1
                                                                                          19-JAN-1994
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               Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a group of linear or cyclic tetra- to decapeptides which include Peptide T and its analogues, where at least one of peptides which include Peptide T and its analogues, where at least one of the amino acids may optionally have a monomeric or polymeric carbohydrate substituted onto a hydroxyl, amino and/or amido group. In one aspect the invention relates to the use of these peptides for the treatment of inflammation; and in another aspect it relates to those peptides in which ceptide T) as new chemical entities. The present peptide is one of 10 specific peptides listed in a sub-claim for use in the treatment of inflammation. The peptides at immunomodulators in the treatment of prevention of inflammation. In particular they can be used in the treatment and propathies and symptoms and diseases associated with chronic immune myopathies in cluding chronic fatigue syndrome, toxic shock, arthritis, inflammatory bowel disease, and host-versus-graft and graft-versus-host responses in transplant recipients. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSP, tropical spastic paresis, HTLV-1, neuromotor; cognitive, HIV; gpl20, replication; AIDS; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New linear and cyclic peptide T analogues - used for treatment and prevention of inflammation, e.g. multiple sclerosis and myelopathies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                Macfadden DK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 41; DB 2; I
; Pred. No. 1.8e+06;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                Carlen PL,
Widmer F;
                                                                                            /note= "D-Thr-NH2"
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                                                                                                                                                                                                                                                                                                                                         (PEPT-) PEPTIDE TECHNOLOGY LTD. (DRUG-) DRUG ROYALTY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
100.0%;
                     /note= "D-Thr"
                                                    /note= "D-Thr"
                                                                                                                                                                                                                                                                                  92US-00915118.
92US-00987674.
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Best Local Similarity 100.vv

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Rathjen D,
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                                         Misc-difference 5
 Misc-difference
                                                                          Misc-difference
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                                                                                                                                 WO9320102-A1
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22-JUN-1994
                                                                                                                                                                                                           29-MAR-1993;
                                                                                                                                                                      14-OCT-1993
                                                                                                                                                                                                                                                 27-MAR-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR47827;
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RESULT 11 AAR47827

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Gaps

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Length 8;

Gaps

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Indels

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The invention relates to a new method of treating eczema or dermatitis using Peptide T and its variants. The present sequence represents one of the preferred variants. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treatment or prevention of eczema or dermatitis, esp. atopic eczema
using specified peptide, e.g the octa:peptide Peptide T.
                                                                                                                                                                                                                                                                                                                                                                                                                                peptide T; prototype; octapeptide; eczema; dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 41; DB 2; L. Llarity 100.0%; Pred. No. 1.8e+06; Conservative 0; Mismatches 0;
  100.0%; Pred. No. 1.8e+06; ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                      Peptide T variant used for treating eczema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "D-form residue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                         AAR59493 standard; peptide; 8 AA.
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(first entry)
                       8; Conservative
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Best Local Similarity
Matches 8; Conserv
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les 8; Conserv
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26-NOV-1995
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Matches
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                                                                                                                                                                                                                                                              The invention relates to a new method of treating eczema or dermatitis using Peptide T and its variants. The present sequence is that of prototype peptide T which is is one of the preferred peptides. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                        Treatment or prevention of eczema or dermatitis, esp. atopic eczema using specified peptide, e.g the octa:peptide Peptide T.
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                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 41; DB 2; Length 8; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide T variant used for treating eczema.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR59487 standard; peptide; 8 AA.
                                                                                                                                                                                                                         Claim 3; Page 14; 20pp; English.
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                     PEPTIDE TECHNOLOGY LTD.
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(first entry)
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                                                            Michaelis J, Trigg TE;
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                                                                                                           WPI; 1995-139385/18
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Matches 8; Conserv
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26-NOV-1995
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RESULT 13 AAR59487

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Length 8;

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Treatment or prevention of Crohn's disease or ulcerative colitis - by use of specified peptide, e.g. Peptide {\bf T}.
                                                     peptide T; prototype; octapeptide; Crohn's disease; ulcerative; colitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a new method of treating or preventing Crohn's disease and/or ulcerative colitis using Peptide T and its variants. The present sequence is one of the preferred peptides. (Updated on 25-MAR-2003 to correct PN field.)
                                 Peptide T variant for use in treating Crohn's disease.
                                                                                                                        'note= "D-form residue"
                                                                                                                                               'note= "D-form residue"
                                                                                                                                                                     'note= "D-form residue"
                                                                                                   Location/Qualifiers
                                                                                                                                                                                           /note= "D-Thr-NH2"
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                                                                                                                                                                                                                                                                                                          (PEPT-) PEPTIDE TECHNOLOGY LTD.
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(revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                  Michaelis J, Sleigh MJ;
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                                                                                                                                    Misc-difference 3
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Misc-difference
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25-MAR-2003
26-NOV-1995
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Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 8; Conservative 0; Mismatches 0; Indels

Search completed: March 18, 2005, 19:10:10 Job time : 80.16 secs

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Sequence 15, Appli
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/cgm2_6/ptodata/1/iaa/6A_COMB.pep:*
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/cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-08-302-829-3
US-08-302-829-10
US-08-481-252-32
US-08-481-840A-1
US-08-481-840A-1
US-08-481-840A-1
US-08-481-840A-3
US-08-403-718-6
US-08-403-718-6
US-08-403-718-6
US-08-619-462-6
US-08-619-462-6
US-09-082-837A-3
US-09-082-837A-3
US-09-082-837A-3
US-09-421-845-3
US-09-421-845-10
US-09-257-490-12
US-09-257-490-12
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Sequence 21372, A Sequence 44250, A Sequence 5, Appli Sequence 5, Appli Patent No. 5276016 Sequence 1, Appli Sequence 1, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli
                                                                                                                                                 Sequence 4, Appendence 2, Appendence 11, Appendence 11, Appendence 11, Appendence 11, Appendence 22190
                                                                                                                                                                                                                                                        Sequence
US-09-248-796A-21372
US-09-270-76-44250
US-08-403-718-5
US-08-619-462-5
5276016-1
US-08-554-758-1
US-08-302-829-2
US-08-302-829-11
US-08-302-829-11
US-08-619-462-4
US-09-082-817A-2
US-09-082-817A-2
US-09-082-817A-11
US-09-421-845-2
US-09-421-845-1
```

# ALIGNMENTS

```
Sequence 4, Application US/07920597
Patent No. 5447915
GENERAL INFORMATION:
APPLICANT: Schreiber, Stuart
APPLICANT: Burakoff, Steven
TITLE OF INVENTION: Terminally-Blocked Antiviral Peptides
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allgretti & Witcoff, Ltd.
STREET: 10 SOUth Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/920,597
FILING DATE: 19920828
CLASSIFICATION NUMBER: US/07/920,597
FILING APPLICATION: 514
PRIOR APPLICATION NUMBER: WO pct/u891/01142
APPLICATION NUMBER: WO pct/u891/01142
APPRINTY/AGENT INPORMATION:
NAME: No. 5447915nan, Kevin E
REGISTRATION NUMBER: 35,303
REFRENCE/DOCKET NUMBER: 91,174-E
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: 312-715-1234
                                                                                                                                                                                                                                                                                                                        ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: peptide US-07-920-597-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                           CITY: Chicase
STATE: IL
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Gaps ö Indels Query Match 100.0%; Score 41; DB 1; Length Best Local Similarity 100.0%; Pred. No. 4.1e+05; Matches 8; Conservative 0; Mismatches 0; Indel

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1 ASTITINYT

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Gaps

; 0

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APPLICANT: ASTON, Roger
APPLICANT: CARLEN, Peter L
APPLICANT: DOOB, Penelope R
APPLICANT: MacFADDAEN, Douglas K
APPLICANT: PHIPPS, David J
APPLICANT: RATHUEN, Deborah
APPLICANT: RATHUEN, Pebride T and Related Peptides in the
TITLE OF INVENTION: Treatment of Inflammation, Including Multiple Sclerosis
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & ALLIACOPPUMP.
STEPPED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 41; DB 1; Length 8; 100.0%; Pred. No. 4.1e+05; Live 0; Mismatches 0; Indels
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OURENTING SYSIEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,829
FILING DATE: 29-MAR-1993
CLASSIFICATION NUMBER: US/08/302,829
FILING DATE: 29-MAR-1993
RIGOR APPLICATION NUMBER: US/08/302,829
FILING DATE: 29-MAR-1993
PRIOR APPLICATION NUMBER: US 07/987,674
FILING DATE: 29-MAR-1993
PRIOR APPLICATION NUMBER: US 07/987,674
FILING DATE: 09-DEC-1992
PRIOR APPLICATION NUMBER: US 07/915,118
FILING DATE: 17-JUL-1992
PRIOR APPLICATION NUMBER: US 07/915,118
FILING DATE: 14-MAY-1992
PRIOR APPLICATION NUMBER: US 07/915,118
FILING DATE: 14-MAY-1992
PRIOR APPLICATION NUMBER: US 07/958,832
FILING DATE: 17-JUL-1992
RILOR APPLICATION NUMBER: US 07/958,832
FILING DATE: 17-MAY-1992
ATTOMEN'AMBER: US 07/958,832
ATTOMEN'AMBER: US 07/958,832
ATTOMEN'AMBER: US 07/958,832
;
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: BANNER & ALLEGRETTI, LTD. 10 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                               Sequence 5, Application US/08302829
Patent No. 5756449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: MCDONNEIL, JOHN J
REGISTRATION NUMBER: 26997
REFRENCE/DOCKET NUMBER: 94,7
TELECOMMUNICATION INFORMATION:
TELEPAK: 312-715-1000
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SS: not relevant circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 amino acids
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: peptide US-08-302-829-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRECT: 10 s.
STREET: 10 s.
CITY: Chicago
                                                 1 ASTTTNYT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                           US-08-302-829-5
    Matches
                                                                                           셤
                                                   ઠ
                                                                                                                                                                                                                                                                                       APPLICANT: DOOB, Penelope R
APPLICANT: MACFADDAEN, Douglas K
APPLICANT: PHIPPS, David J
APPLICANT: PHIPPS, David J
APPLICANT: RATHJEN, Deborah
APPLICANT: RATHJEN, Deborah
APPLICANT: WIDMER, Fred
TITLE OF INVENTION: Peptide T and Related Peptides in the
TITLE OF INVENTION: Treatment of Inflammation, Including Multiple Sclerosis
CORRESPONDENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CUMPURY: USA

CUDNIKY: USA

CUDNIKY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/302,829

FILING DATE: 29-MAR-1993

CLASSIPICATION: DATA:

APPLICATION NUMBER: WO PCT/GB93/00649

FILING DATE: 29-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/987,674

FILING DATE: 19-AUL-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/915,118

FILING DATE: 11-AUL-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/915,118

FILING DATE: 14-MAY-1992

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US 07/915,118

FILING DATE: 14-MAY-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/858,832

FILING DATE: 27-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 1;
Pred. No. 4.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1..8

CTHER INFORMATION: /note= "Ala 1 is D-Ala"
US-08-302-829-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BANNER & ALLEGRETTI, LTD
                                                                                                                                          Sequence 3, Application US/08302829
Patent No. 5756449
GENERAL INFORMATION:
APPLICANT: ANDERSEN, Anders J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 26949
REFERENCE/DOCKET NUMBER: 94,7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1034
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 10 S. Wacker Drive CITY: Chicago STATE: Illinois COUNTRY: USA
                                                                                                                                                                                                                                             ASTON, Roger
CARLEN, Peter L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: McDonnell, John J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: both
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
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1 ASTITNYT 8
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Best Local Similarity
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US-08-302-829-3
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Gaps

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US-08-488-252-32

Sequence 32, Application US/08488252

Sequence 32, Application US/08488252

Patent No. 5763160

Patent No. 5763160

TITLE OF INVENTION: SYNTHETIC PEPTIDES AND PROCESS

TITLE OF INVENTION: OF USING SAME FOR THE DETECTION OF ANTIBODIES TO

TITLE OF INVENTION: PROTEIN, DIAGNOSIS OF AIDS AND PRE-AIDS CONDITIONS

TITLE OF INVENTION: AND AS VACCINES

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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  Length 8;
    100.0%; Score 41; DB 1; I 100.0%; Pred. No. 4.1e+05;
                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1151-4004 US4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08\326,676

FILING DATE: 07-Jun-1995

APPLICATION NUMBER: 07\726,605

FILING DATE: 09-July-1991

APPLICATION NUMBER: 07\63,262

FILING DATE: 01-Max-1991

APPLICATION NUMBER: 07\63,262

FILING DATE: 12-Feb-198

APPLICATION NUMBER: 29\321

FILING DATE: 11-Feb-198

APPLICATION NUMBER: 29\321

REGISTATION NUMBER: 29\321

REGISTATION NUMBER: 29\321

REFERENCE/DOCKET NUMBER: 1151-400

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECHONE: 212-758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVE.
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY I
Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASTTTNYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-488-252-32
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                                                                                                                                                                    APPLICANT: ASTON, Roger

APPLICANT: ASTON, Roger

APPLICANT: CARLEN, Peter L

APPLICANT: CARLEN, Peter L

APPLICANT: MACFADDEN, Douglas K

APPLICANT: MACFADDEN, Douglas K

APPLICANT: PITPES, David J

APPLICANT: WIDMER, Pred

TITLE OF INVENTION: Preptide T and Related Peptides in the

TITLE OF INVENTION: Treatment of Inflammation, Including Multiple Sclerosis

CORRESPONDENCE ADDRESS:

ADDRESSEE: BANNER & ALLEGRETTI, LTD

CORRESPONDENCE ADDRESS:

ADDRESSEE: BANNER & ALLEGRETTI, LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "aal is D-Ala, aa3 is D-Thr,
aa5 is D-thr, aa8 is D-Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

KNEIULM TYPE: 18M PC compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/302,829
FILING DATE: 29-MAR-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: WO PCT/GB93/00649
FILING DATE: 29-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/987,674
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/915,118
FILING DATE: 17-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/858,832
FILING DATE: 20-MAR-1993
PRIOR APPLICATION NUMBER: US 07/858,832
FILING DATE: 21-MAR-1992
PRIOR APPLICATION NUMBER: US 07/858,832
FILING DATE: 21-MAR-1993
APPLICATION NUMBER: 26949
FILING DATE: 21-MAR-1992
APPLICATION NUMBER: 26949
FILING DATE: 21-MAR-1992
ATTORNEY/ASRIT INFORMATION:
TELEPHONE: 312-715-1234
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: Amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: BANNER & ALLEGRETTI, LTD. STREET: 10 S. Wacker Drive CITY: Chicago STATE: Illinois COUNTRY: USA
                                                                                                                                                               Sequence 10, Application US/08302829
Patent No. 5756449
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: both
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: Peptide
; LOCATION: 1.8
; OTHER INFORMATION: ;
US-08-302-829-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     both
                                                                                                                                              US-08-302-829-10
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Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 41; DB 1; I Best Local Similarity 100.0%; Pred. No. 4.1e+05; Matches 8; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08481840A

Patent No. 5763406

GENERAL INFORMATION:
APPLICANT: PEDERSEN, Ove
APPLICANT: PEDERSEN, D.
TITLE OF INVENTION: Peptides for Treatment
NUMBER OF SEQUENCES: 7
CORRESSEN: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive
CITY: Chicago
STATE: 111inois
COUNTRY: 10 South Wacker Drive
CITY: READABLE FORM:
MEDIUM TYPE: Floppy Disk, 3.50 inch
COMPUTER: BM PC Compatible
OPERATION SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/107,777
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: INANICALION DATA:
APPLICATION NUMBER: 34,628
REGISTRATION NUMBER: 34,628
REGISTRATION NUMBER: 34,628
REGISTRATION NUMBER: 34,628
REGISTRATION NUMBER: 34,628
REFERENCE/DOCKET NUMBER: 33,71-A
TELEDHONE: 617-345-910
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/481,840A
FILING DATE: US-08/481,840A
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/107,777
FILING DATE: 24-NOV-1993
ATTORNEY AGENT INPORMATION:
NAME: IWANICKI, JOHN P
REGISTATION NUMBER: 34,628
REFERRNCE/DOCKET NUMBER: 34,741-A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHAN: 617-345-910
TELEFRX: 617-345-910
TINFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 8 amino acids
TYPE: amino acids
STRANDENESS:
TOPOLOGY: Linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ASTITINI 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-481-840A-2
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JOS-08-481-840-2

JOS-08-481-840-2

JOSEQUANCE 2, Application US/08481840A

Patent No. 5763406

GENERAL INFORMATION:

APPLICANT: PEDERSEN, Ove

APPLICANT: MACFADDEN, D.

TITLE OF INVENTION: Peptides for Treatment

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Allegrett, Ltd.

STREET: 10 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk, 3.50 inch

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

SOFTWARE: WordPerfect 6.1
         US-08-481-840A-1

Sequence 1, Application US/08481840A

Patent No. 5763406

JEANT PEDERSEN, Ove

APPLICANT: MACRADDEN, D.

TITLE OF INVENTION: Peptides for Treatment
NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSE: ADDRESSE:

ADDRESSE: Banner & Allegretti, Ltd.

STREET: 10 South Wacker Drive

CITY: Chicago

STREET: 111inois

STRIET: 111inois

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                       ZIP: 66606
COMPUTER READMBLE FORM:
MEDIUM TYPE: Floppy Disk, 3.50 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,840A
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/107,777
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Iwanicki, John P
REGISTRATION NUMBER: 34,628
REFERENCE/DOCKET NUMBER: 33,741-A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAN: 617-345-9111
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acid8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 8; Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-481-840A-2
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0; Gaps

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Sequence 1. Application US/08619462

Patent No. 5798335

GENERAL INFORMATION:
APPLICANT: MICHAELIS, JURGEN
APPLICANT: Trigg, Timothy Elliot
ITILE OF INVENTION: ECZEMA/DERMATITIS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE BUBRES:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                     STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,718
FILING DATE: JA-MAR.1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/619,462
FILING DATE: 07-MAY-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 41; DB 1; I 100.0%; Pred. No. 4.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                         VANDERHYE P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MITCHARD, LEONARD C.
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 47-84
TELECOMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                         ADDRESSEE: NIXON & VANDERHYE E
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: MITCHARD, LEONARD C.
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 47-7;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-400
TELEFAX: (704) 816-4100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 100...
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 8 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ASTITINYT 8
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US-08-619-462-1
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                                                                                                                                                                                                                                                                        Sequence 1, Application US/08403718;
Patent No. 5795858;
GENERAL INFORMATION:
APPLICANT: MICHAELIS, JURGEN
APPLICANT: SIEIGH, MERLINN J.
TITLE OF INVENTION: TREATMENT OR PREVENTION OF CROHN'S
TITLE OF INVENTION: DISEASE AND/OR ULCERATIVE COLITIS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                            100.0%; Score 41; DB 1; Length 8; 100.0%; Pred. No. 4.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 41; DB 1; Length 8; 100.0%; Pred. No. 4.1e+05;
                                                                                                    0; Indels
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Patent No. 5795688
GENERAL INFORMATION: TREATMEN J.
APPLICANT: SLEIGH, MERILYN J.
TITLE OF INVENTION: TREATMENT OR PREVENTION OF CROHN'S
TITLE OF INVENTION: DISEASE AND/OR ULCERATIVE COLITIS
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/403,718

FILING DATE: 31-MAR-1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: MITCHARD, LEONERD C.

REGISTRATION NUMBER: 29,009

REGISTRATION NUMBER: 29,009

REGISTRATION INFORMATION:

TELEFANCE, (703) 816-4000

ITELEFAN: (704) 816-4000

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 mmino acids

LENGTH: 8 mmino acids
                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
                                                        Query Match 100.
Best Local Similarity 100.
Matches 8; Conservative
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MOLECULE TYPE: peptide
US-08-403-718-1
MOLECULE TYPE: peptide
                                                                                                                                          1 ASTTTNYT 8
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      US-08-403-718-1
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US-08-403-718-6
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Gaps

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GENERAL INFORMATION:
APPLICANT: YEN, R
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US-06-619-462-6
i Sequence 6, Application US/08619462
i Sequence 6, Application US/08619462
i Patent No. 5798335
i GARREAL INFORMATION:
APPLICANT: MICHABLIS, JURGEN
APPLICANT: Trigg, Timothy Elliot
ITLE OF INVENTION: REZEMA/DERMATITIS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ALLINGTON
STATE: VIRGINIA
COUNTY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATA: Release #1.0, Version #1.30
CURRENT APPLICATION NATA: APPLICATION DATA: APPLICATION NUMBER: US/08/619,462
FILLING DATE: 07-MAY-1996
CLASSIFICATION: 514
ATTORREYARD: INFORMATION:
NAME: MITCHARD, LEGNARD.
SEGIENCE/DOCKET NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 47-84
TELEFONMATICN TON SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LEMCTH: 8 mainto acids
LENCTH: 8 mainto acids
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                                                                                                                                                                                Length 8;
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                                                                                                                                                                                100.0%; Score 41; DB 1; I 100.0%; Pred. No. 4.1e+05;
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US-08-747-137-20
; Sequence 20, Application US/08747137
TELEFAX: (704) 816-4100 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
                                                                                                                                                                                               Best Local Similarity 100.
Matches 8; Conservative
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                                                       LENGIH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-619-462-6
                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-619-462-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid STRANDEDNESS:
                                                                      TYPE: amino acid STRANDEDNESS:
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                                                                                                                                                                                  Query Match
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Sequence 3, Application US/09082837A

Sequence 3, Application US/09082837A

Sequence 10. 6011014

GENERAL INFORMATION:
APPLICANT: ANDERSEN, Anders J

APPLICANT: CARLEN, Peter L

APPLICANT: DOOB, Penelope R

APPLICANT: PHIPPS, David J

APPLICANT: RAITHEN, Deborah

APPLICANT: RAITHEN, Peptide T and Related Peptides in the Treatment of TITLE OF INVENTION: Inflammation, Including Multiple sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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0
APPLICANT: YEN, Richard C.K.
TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE
NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
STORMEST: Two Sembarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 8;
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                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Plan PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NAMER: US/08/747,137
FILING DATE: 12-NOV-1996
CLASSIFICATION NAMER: US 08/212,546
FILING DATE: 14-MAR-1994
FILING DATE: 14-MAR-1994
FILING DATE: 01-JUN 1993
APPLICATION NUMBER: US 07/959,560
FILING DATE: 13-OCT-1992
RAPLICATION DATA:
APPLICATION NUMBER: US 07/959,560
FILING DATE: 13-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/959,560
FILING DATE: 15-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: APPLICATION NUMBER: 016197-000840US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 41; DB 2; I
100.0%; Pred. No. 4.1e+05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: not relevant US-08-747-137-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 415-576-0200
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ASTTTNYT
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APPLICANT: RATHER, becard
APPLICANT: MITES, Lavya J
TITLE OF INVENTION: Inflammation, Including Multiple sclerosis
CORRESPONDENCE ADDRESS:
ADDRESSES: ADDRESS:
ADDRESSES: BANNER & HITCOPP, LTD.
CITY. Chicago
CITY: Chicago
CITY: Chicago
COMPUTER: Inhois
COMPUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 41; DB 3; Length 8; Best Local Similarity 100.0%; Pred. No. 4.1e+05; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: March 18, 2005, 19:12:09 Job time : 20.52 sec8
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      PHIPPS, David J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: not releve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: circular
MOLECULE TYPE: peptide
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1 ASTTTNYT
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                                                                                                                                                                COMPUTER: USA

ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BATCHIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,837A
FLING DATE: 21-JUN-1998
CLASSIPICATION NUMBER: US 08/302,829
FLING DATE: 29-MAR-1993
RRIOR APPLICATION NUMBER: WO PCT/GB93/00649
FLIING DATE: 29-MAR-1993
RRIOR APPLICATION NUMBER: WO PCT/GB93/00649
FILING DATE: 29-MAR-1993
RRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/987,674
FILING DATE: 17-JUL-1992
RRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,118
FILING DATE: 37-MAR-1992
RRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/986,832
FILING DATE: 27-MAR-1992
RRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/858,832
FILING DATE: 27-MAR-1992
RRIOR APPLICATION NUMBER: US 07/858,832
FILING DATE: 37-MAR-1992
RRIOR APPLICATION NUMBER: US 07/858,832
FILING DATE: 37-MAR-1992
RRIOR APPLICATION NUMBER: US 07/858,832
FILING DATE: 37-MAR-1993
REFERENCE DOCKET NUMBER: 27-93
REFERENCE DOCKET NUMBER: 27-000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-712-1000
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100.0%; Pred. No. 4.1e+05;
tive 0; Mismatches 0;
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; OTHER INFORMATION: /note= "Ala 1 is D-Ala"
US-09-082-837A-3
                             ADDRESSEE: BANNER & WITCOFF, LTD. STREET: 10 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09082837A
Patent No. 6011014
GENERAL INFORMATION:
APPLICANT: ASTON, Roger
APPLICANT: CARLEN, Peter L
APPLICANT: CARLEN, Peter L
APPLICANT: MacFADDAEN, Douglas K
APPLICANT: MacFADDAEN, Douglas K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: both
MOLECULE TYPE: peptide
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Peptide
                                                                                        Chicago
: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                     STATE: I
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US-09-082-837A-5
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March 18, 2005, 19:02:16; Search time 58.88 Seconds (without alignments) 44.910 Million cell updates/sec
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| Cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.ppp: *
| Cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.ppp: *
| Cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.ppp: *
| Cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.ppp: *
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| Cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.ppp: *
| Cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.ppp: *
| Cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.ppp: *
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| Cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.ppp: *
| Cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.ppp: *
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1401741 seqs, 330541175 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published_Applications_AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
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                                                                                                                                                                                                                                                                                                 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

8822.23	104 104 358 759	122	US-09-925-299-1516 US-09-925-299-1516 US-10-767-701-40122 US-10-449-857A-88 US-10-618-581-38 US-10-451-467A-364	Sequence 1516, Ap Sequence 1516, Ap Sequence 88, Appl Sequence 88, Appl Sequence 38, Appl	6, Ap 22, A Appl Appl App
80.9	118	15	US-10-424-599-207321 US-10-424-599-263645	Sequence 207	207321, 263645.
	8888888 8228888 926888888		104 16 358 15 759 15 118 15	104 16 358 15 759 15 118 15	104 16 US-10-767-701-40122 358 15 US-10-449-857A-88 759 15 US-10-618-581-38 759 16 US-10-451-467A-364 118 15 US-10-454-599-207321 333 15 HG-10-47A-809-207321

RESULT 2

Sequence 46985, A Sequence 41218, A Sequence 61234, A Sequence 951, App Sequence 951, App Sequence 22341,	Sequence Sequence Sequence Sequence Sequence Sequence	Sequence 55428, A Sequence 1590, Ap Sequence 1590, Ap Sequence 13489, Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli	
US-10-767-701-46985 US-10-425-114-43218 US-10-425-114-63234 US-09-764-847-951 US-10-092-154-951 US-10-424-599-223447 US-09-910-150-29	US-10-377-097-29 US-09-910-150-28 US-10-377-097-28 US-10-237-097-28 US-10-437-963-176857 US-09-244-984-5	US-10-425-114-5548 US-10-425-114-5548 US-10-774-355A-1590 US-10-295-027-356 US-09-727-169-4 US-09-727-169-4 US-09-728-968-4	US-10-423-729-4 US-10-437-663-123816 US-10-369-493-8983 US-09-727-169-2 US-09-726-968-2 US-10-281-478-1 US-10-295-027-354 US-10-156-761-7751 US-10-149-135-242 US-10-149-135-242
15 15 15 15 15 15	2 6 1 1 1 2 6 7	41 11 12 13 14 15 15 16 17	446466
44 4 4 8 8 3 4 4 4 6 9 2 9 2 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	11111111111111111111111111111111111111	2 2 3 3 3 3 3 4 5 8 6 9 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	2000 8800 8800 8800 8800 8800 8800 8800
80.5 80.5 80.5 78.0 78.0	78.0 78.0 78.0 78.0	78.0 78.0 78.0 78.0 78.0	78.0 78.0 78.0 78.0 78.0 78.0 75.6
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# ALIGNMENTS

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US-10-062-710-230
US-10-062-710-12
UNUBER OF INVENTION: Via Peptide Vaccines
US-10-062-710
UUSERT APPLICATION NUMBER: US/10/062,710
UURERNT APPLICATION NUMBER: US/10/062,710
UURERNT FILING DATE: 2001-08-08
UUMBER OF SEQ ID NOS: 232
UNUMBER OF SEQ ID NOS: 232
UNUMBER OF SEQ ID NOS: 232
USCTWARE: FastSEQ for Windows Version 4.0
USEQ ID NOS: 232
USG ID NOS: 232
USG
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OTHER
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                                                                                                   APPLICANT: Hara, Toshio
TITLE OF INVENTION: Nucleic Acid Capable of Promoting Gene Expression
FILE REFERENCE: 027847, 00102US01
CURRENT APPLICATION NUMBER: US/10/361,849
CURRENT FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: 60/355,752
PRIOR APPLICATION NUMBER: 06/355,752
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.2
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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US-210-8/2-198-129

Publication No. US2005002897A1

GENERAL INFORMATION:

APPLICANT: Ulrich HAUDTS

APPLICANT: Ulrich HAUDTS

APPLICANT: Andreas SCHEIDIG

APPLICANT: Andreas SCHEIDIG

APPLICANT: Christian VOETSMEIRR

APPLICANT: Christian VOETSMEIRR

APPLICANT: Ulrich Kettling

TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF

FILE REFERENCE: 04156.0002U4

CURRENT APPLICATION NUMBER: US/10/872,198

CURRENT FILING DATE: 2004-02-11

PRIOR PELING DATE: 2004-02-11-25

PRIOR APPLICATION NUMBER: EP 04003058

PRIOR APPLICATION NUMBER: EP 04003058

PRIOR PELING DATE: 2003-11-10

PRIOR FILING DATE: 2003-11-10

PRIOR FILING DATE: 2003-11-10

PRIOR PELING DATE: 2003-11-10

PRIOR PELING DATE: 2003-11-10

PRIOR PELING DATE: 2003-11-10

PRIOR APPLICATION NUMBER: EP 03013819

PRIOR FILING DATE: 2003-11-10

PRIOR PELING DATE: 2003-11-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 41; DB 14; Length 451; 100.0%; Pred. No. 23; tive 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Human immunodeficiency virus
US-10-361-849-15
                  Sequence 15, Application US/10361849
Publication No. US20030170619A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 ASTITINYT 134
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Best Local Similarity
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US-10-361-849-15
                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM:
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RESULT 4 US-10-424-599-166162

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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Ea Rosa Thomas J
APPLICANT: Abou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 166162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAA02

CURRENT APPLICATION NUMBER: US/09/925,299

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05883

PRIOR PILING DATE: 2000-03-08

PRIOR PILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1556

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_12105C.1.pep
US-10-424-599-166162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35; DB 15;
Pred. No. 72;
0; Mismatches 1
Sequence 166162, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1516, Application US/09925299 Patent No. US20020055627A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85.4%;
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Best Local Similarity 87.5
Matches 7; Conservative
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OTHER INFORMATION: Xaa
NAME/KEY: SITE
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OTHER INFORMATION: Xaa
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OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            || |||||
83 ASITTNYT 90
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US-10-618-581-38
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GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yonguic
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

    LOCATION: (52)
    OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1516

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Sequence 1516, Application US/09925299

Sequence 1516, Application US/09925299

Hublication No. US20030040617A9

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

TITLE REFERENCE: PA102

CURRENT APPLICATION NUMBER: US/09/925,299

CURRENT FILING DATE: 2001-08-10

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1556

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1516
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Score 34; DB 9; Length 66;
Pred. No. 59;
1; Mismatches 1; Indels
Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
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57 SKTTTNYT 64
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57 SKTTTNYT 64
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Best Local Similarity
Matches 6; Conserva
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Sequence 88, Application US/10449857A

Publication No. US20040043931A1

GENERAL INFORMATION:

APPLICANT: Hosken, Nancy A.

APPLICANT: Lodes, Michael J.

APPLICANT: Mohamath, Raddoh

TITLE OF INVENTION: AND DIAGNOSIS OF INFLAMMATORY BOWEL DISEASE

FILE OF INVENTION: AND DIAGNOSIS OF INFLAMMATORY BOWEL DISEASE

FILE REFERENCE: 584C1

CURRENT FILING DATE: 2003-05-30

NUMBER OF SEQ ID NOS: 89

SOFTWARE: Corixa Invention Disclosure Database

LENGTH: 358

TYPE: PRT

ORGANISM: Unknown
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APPLICANT: WANNING, GERARD
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: METHOD FOR SELECTIVELY INHIBITING FUNGAL GROWTH
FILE REFERENCE: 034536/0323
CURRENT APPLICATION NUMBER: US/10/618,581
PRIOR APPLICATION NUMBER: 60/395,624
PRIOR PELICH DATE: 2002-07-15
PRIOR PELICH DATE: 2002-07-15
SOFTWARE: PACENTIN NOW: 42.
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85.7%; Pred. No. 93;
tive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C5227_1.pep
US-10-767-701-40122
                                                                                                                                                                                                           LOCATION: (1)...(104)
OTHER INFORMATION: unsure at all Xaa locations
PEATURE:
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 40122
LENGTH: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Unknown Bacterium
US-10-449-857A-88
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Publication No. US20040077524A1
GENERAL INFORMATION:
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                     TYPE: PRT ORGANISM: Sorghum bicolor
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238 SDTTTNYT 245
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Best Local Similarity
'''na 6, Conserve
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Gequence 233645, Application US/10424599

Squence 233645, Application US/10424599

Gentance 233645, Application No. US2004003107241

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Chou Yihua
APPLICANT: Cao Yongwei.
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 263645

LENGTH: 233
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APPLICANT: Zhou, Yibonia
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 40777
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                                    80.5%; Score 33; DB 15; Length 118; 85.7%; Pred. No. 1.6e+02; ive 1; Mismatches 0; Indel8
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US-10-424-599-263645
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US-10-425-114-40777
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                   Query Match
Best Local Similarity 85...
6; Conservative
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113 ASSSTNYT 120
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108 STSTNYT 114
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US-10-424-599-263645
US-10-424-599-207321
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Abou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 207321
SEQ ID NO 207321
                                                                                                                                                                                                                                                                                                                                              RESULT 10

US-10-451-467A-364

i Sequence 364, Application US/10451467A

i Sequence 364, Application US/10451467A

i Publication No. US20040161840A1

GENERAL INFORMATION:

APPLICANT: CONTERAS, ROLAND HENRI

APPLICANT: LUYTEN WALTER HERMAN MARIA LOUIS

APPLICANT: LUYTEN WALTER HERMAN MARIA LOUIS

APPLICANT: REERAMANS, REEKA JOSEPHINA

TITLE OF INVENTION: YEAST AND FUNG!

TITLE OF INVENTION: YEAST AND FUNG!

TITLE OF INVENTION: YEAST AND FUNG!

CURRENT APPLICATION NUMBER: US/10/451,467A

CURRENT PILING DATE: 2003-06-19

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2001-01-04

PRIOR FILING DATE: 2001-01-09

NUMBER OF SEQ ID NOS: 732

SEQ ID NO 364

LENGTH: 759

LENGTH: 759
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Best Local Similarity 85.7%; Pred. No. 6.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels
                                                                                                                                     82.9%; Score 34; DB 15; Length 75
85.7%; Pred. No. 6.9e+02;
.ive 1; Mismatches 0; Indels
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; SEQ ID NO 38
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-618-581-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Saccharomyces cerevisiae
                                                                                                                                            Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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64 TTTTNYT 70
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64 TTTTNYT 70
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RESULT 14
US-10-767-701-46985
; Sequence 465965, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21 (53555) B
; CURRENT APPLICATION NUMBER: US/10/767,701
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 46985
; LENGTH: 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-425-114-43218

Sequence 43218, Application US/10425114

Publication No. US20040034888A1

Sequence 43218, Application No. US2004003488BA1

Sequence 43218, Application No. US2004003488BA1

APPLICANT: Dio, Jingdong

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

WUMBER OF SEQ ID NOS: 73128

SEQ ID NO 43218

LENGTH: 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80.5%; Score 33; DB 16; Length 476; 100.0%; Pred. No. 6.5e+02; Live 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C49_319.pep
US-10-767-701-46985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: LIB3067-008-A2_FLI.pep
US-10-425-114-43218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Sorghum bicolor
||::||||
117 ASSSTNYT 124
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Search completed: March 18, 2005, 19:15:20 Job time : 59.88 secs

107 TTTNYT 112

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GenCore version 5.1.6
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                 Copyright
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sw model protein search, using OM protein

Run on:

March 18, 2005, 18:59:20 ; Search time 15.68 Seconds (without alignments) 49.090 Million cell updates/sec

US-10-773-274A-1

1 ASTTTNYT 8 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 88 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	env polyprotein pr	hypothetical prote	conserved hypothet	probable serralysi		NADH2 dehydrogenas	probable membrane	capB protein - Clo	ferric-pseudobacti	hypothetical prote	probable 0-acetylt	FimH protein precu	Α.	hypothetical prote								•	melanoma antigen M	protein F56E10.3 [	hypothetical prote	nuclear localizati			
SUMMARIES	ΩI	VCLJA2	T33404	G69212	H95263	QQBE34	T11507	S67164	S57714	S15169	T21389	850709	AC0570	H88639	T32533	T23181	T24690	E89772	T27473	VGBEMC	E86719	T03136	D97858	I68889	F88921	T19359	T40924	S48471	T30374	F97279
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. <b>de</b>	Query Match	100.0	90.5	87.8	85.4	85.4	82.9	82.9	80.5	80.5	80.5	78.0	78.0	78.0	78.0	78.0	78.0	78.0	78.0	78.0	78.0	75.6	75.6	75.6	75.6	73.2	73.2	73.2	73.2	73.2
	Score	41	37	36	35	35	34	34	33	33	33	32	32	32	32	32	32	32	32	32	32	31		31	31	30	30	30	30	30
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probable G2-specif	probable sensory h homeotic protein H	peptidoglycan boun	adhesin homolog lm	toxin-like outer m	hypothetical prote	Ig heavy chain V r	hypothetical prote	hypothetical prote	٠.			probable sugar ABC	hypothetical prote	
T37970	F95884 S65774	AD1512	AC1153	B64635	D81044	S54912	G84629	E84629	T28297	B90125	E90493	B95884	T37136	T47198
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30	37 32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

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env polyprotein precursor - human immunodeficiency virus type 1 (isolate ARV-2) N;Alternate names: coat polyprotein C;Species: human immunodeficiency virus type 1, HIV-1

C;Accession: A03976
R;Sanchez-Pescador, R:; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-Sh
Science 227, 484-492, 1985
A;Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).
A;Reference number: A04003; MUID:85090453; PMID:2578227

A;Accession: A03976 A;Molecule type: DNA A;Residues: 1-855 <SAN>

A;Cross-references: UNIPROT:P03378; GB:K02007; NID:g328658; PIDN:AAB59882.1; PID:g328666

C; Superfamily: type E retrovirus env polyprotein

C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot F;1-30/Domain: signal sequence #status predicted <SIG> F;31-509/Product: exterior membrane glycoprotein #status predicted <EXT> F;31-509/Product: transmembrane glycoprotein #status predicted <TMM> F;87,129,140,184,184,190,200,244,265,292,298,304,334,341,358,364,388,394,400,408,445,458 F;610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted

Gaps 100.0%; Score 41; DB 1; Length 855; 100.0%; Pred. No. 2.8; cive 0; Mismatches 0; Indel8

ö Query Match
Best Local Similarity 100...

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hypothetical protein H10E21.3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004

C; Accession: T33404
R; Davidson, S.; Wohldmann, P.; Courtney, L.
submitted to the EMBL Data Library, July 1998
A; Description: The sequence of C. elegans cosmid H10E21.
A; Reference number: Z21339

A;Accession: T33404 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA

A;Cross-references: UNIPROT:QBITW8; EMBL:AF078783; PIDN:AAC26921.1; GSPDB:GN00021; CBSP::A;Experimental source: strain Bristol N2; clone H10E21 C;Genetics: A;Residues: 1-504 <DAV>

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A;Accession: F43043
A;Molecule type: DNA
A;Residues: 1-809 <BAN>
A;Cross-references: UNIPROT:P03214; EMBL:V01555; NID:959074; PIDN:CAA24821.1; PID:913348|
B;Cross-references: UNIPROT:P03214; EMBL:V01555; NID:959074; PiDN:CAA24821.1; PID:913348|
B;Back, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; Hi
Nature 310, 207-211, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C,accession: T11507
R;Arcason, U.; Gullberg, A.; Janke, A.
R;Arnason, U.; Gullberg, A.; Janke, A.
J. Mol. Evol. 47, 718-727, 1998
A;Title: Molecular timing of primate divergences as estimated by two non-primate calibra A;Reference number: Z17277; MUID:99065765; PMID:9847414
A;Accession: T11507
A;Accession: T11507
A;Accession: T1807
A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: human herpesvirus 4, Epstein-Barr virus C;Species: 25-Peb-1985 #sequence revision 25-Peb-1985 #text_change 09-Jul-2004 C;Accession: F43043; A03776; §33026 B;A;Bankier, A.T.; Delninger, P.L.; Farrell, P.J.; Barrell, B.G. Mol. Biol. Med. 1, 21-45, 1983 A;Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus A;Reference number: A93065; MUID:85035713; PMID:6092825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: UNIPROT: 09ZXY3; EMBL: Y18001; NID: 94049475; PIDN: CAA76995.1; PID: 9404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Genome: mitochondrion
A,Genetic code: SGC1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - baboon mitochondrion (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome. A;Reference number: A03794; MUID:84270667; PMID:6087149
A;Contents: annotation; protein coding region C;Superfamily: varicella-zoster virus gene 55 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C,Species: mitochondrion Papio hamadryas (baboon)
C,Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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DB 2; Length 551;
27;
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Pred. No. 40;
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7
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Pred. No. 27;
1; Mismatches
                                                                                                                                         0; Mismatches
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                                                  Score 35;
Pred. No. 2
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                                                      85.4%;
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Best Local Similarity 87.5%;
Matches 7; Conservative
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Best Local Similarity 85.,
6, Conservative
                                                  Query Match
Best Local Similarity 87.5
Matches 7; Conservative
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C; Species: Sinorhizobium meliloti
C; Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C; Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C; Accession: H95263
R; Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe
I; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
A; Recession: H95263
A; Recession: H95263
A; Accession: H95263
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A; Residues: 1-551 - KUR>
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A; Residues: 1-556 - KUR>
A; Residues: 1-557 - KUR>
A; Residues: Residues:
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C; Species: Methanobacterium thermoautotrophicum
C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C; Accession: 65212
R; Minith, D.R; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J; Bacteriol. 179, 7135-7155, 1997
A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A; Reference number: A69000; MUD: 98037514; PMID: 9371463
A; Accession: 669212
A; Accession: A; Astaus: preliminary; nucleic acid sequence not shown; translation not shown
A; Mesidues: 1-283 «MTH»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:026933; GB:AE000861; GB:AE000666; NID:g2621930; PIDN:AAB8534 A;Experimental source: strain Delta H C;Genetics: A;Gene: WTH845
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                                                                                                                                                                                                Length 504;
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87.5%; Pred. No. 8.9;
iive 0; Mismatches 1
                                                                                                                                                                                                    7
                                                                                                                                                                                           90.2%; Score 37; DB
larity 87.5%; Pred. No. 10;
Conservative 1; Mismatches
                                                                         A;Map position: 3
A;Introns: 78/1; 168/3; 241/3; 384/1; 434/3
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A,Genome: plasmid
C,Keywords: hydrolase; metalloproteinase
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Best Local Similarity 8/...
7; Conservative
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Best Local Similarity
Matches 7; Conserv
                      A; Gene: CESP: H10E21.3
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C;Species: Pseudomonas putida
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: 515169
C;Accession: 515169
Mol. Microbiol. 5, 647-655, 1991
A;Title: The ferric-pseudobactin receptor PupA of Pseudomonas putida WCS358: homology to
A;Reference number: 515169; MUID:91260449; PMID:1646376
A;Accession: 515169
A;Accession: 515169
A;Accession: 515169
A;Reidiues: 1-619 cBIT>
A;Cross-references: UNIPROT: P25184; EMBL:X56605; NID:g45722; PIDN:CAA39942.1; PID:g45723
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C;Superfamily: ferric-pseudobactin receptor; tonB-dependent receptor amino-terminal homo
C;Superfamily: ferric-pseudobactin predicted <8IG>
F;14-47/Domain: signal sequence #status predicted <8IG>
F;48-819/Product: ferric-pseudobactin receptor #status predicted <WAT>
F;189-322/Domain: tonB-dependent receptor amino-terminal homology <TNN>
F;542-819/Domain: tonB-dependent receptor carboxyl-terminal homology <TNC>
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A;Molecule type: DNA
A;Residues: 1.1251 <WIL>
A;Residues: 1.1251 <WIL>
A;Cross=references: UNIPROT:009550; EMBL:Z47072; PIDN:CAA87369.1; GSPDB:GN00020; CESP:FZ
A;Experimental source: clone F26C11
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21389
R;Matthews, P.
Submitted to the EMBL Data Library, December 1994
A;Reference number: Z19416
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80.5%; Score 33; DB 2; Length 819;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                     ferric-pseudobactin receptor precursor - Pseudomonas putida
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376 TTTNYT 381
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                                    3 TTTNYT 8
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N'Alternate names: hypothetical protein 05420
C'Species a Saccharowyces cerevisiae
C'Checesion: Saccharowyces cerevisiae
C'Accession: S67164, 56716; 572039
R'Accession: S67164, 56716; 572039
R'Accession: S67164, 56716; 572039
R'Accession: S67164
A'Residues: 1-759 -AMJUS
A'Residues: 1-750 -AMJUS
A'Reference number: S67169
A'Residues: 1-367 -CMED
A'Reference number: S67169
A'Reference number: S67169
A'Reference number: S67169
A'Reference number: S67169
A'Residues: 1-367 -CMED
A'Reference number: S70039; MUID: 97051534; PMID: 8996271
A'Reference number: S70039; MUID: 97051534; PMID: 8996271
A'Reference number: S700005793
A'Reference number: S7000005793
A'Reference number: S7000005793
A'Reference number: S7000005793
A'Reference number: S7000005793
A'Reference S7000000790
C'SUpperfamily: protein kinase homology
C'Supperfamily: protein kinase homology
C'Supperfamily: protein kinase homology
C'Supperfamily: protein kinase homology
C'Supperfamily: protein kinase ATP-binding motif
F7.313-456/Domain: transmembrane protein kinase ATP-binding motif
F7.400-416/Domain: transmembrane prot
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A;Residues: 1-635 <SAN>
A;Residues: 1-635 <SAN>
A;Cresidues: 1-635 <SAN>
A;Cresidues: 1-635 <SAN>
A;Cresidues: 1-635 <SAN
A;Cresi
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85.7%; Pred. No. 60;
ive 1; Mismatches 0; Indels
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserva
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Score 32;
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Best Local Similarity 75.0%;
Matches 6; Conservative
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145 ATTTTTYT 152
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                 A,Status: preliminary
A;Molecule type: DNA
A;Residues: 1-340 <STO>
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                                                                                                            A; Accession: H88639
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R; Vandenbol, M.; Durand, P.; Bolle, P.A.; Dion, C.; Portetelle, D.; Hilger, F.
Yeast 10, 1657-1662, 1994
A; Title: Sequence analysis of a 40.2 kb DNA fragment located near the left telomere of y
A; Title: Sequence analysis of a 40.2 kb DNA fragment located near the left telomere of y
A; Title: Sequence analysis of a 40.2 kb DNA fragment located near the left telomere of y
A; Accession: S50709
A; Accession: S50709
A; Accession: S50709
A; Reference unucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-196 «VMN>
A; Residues: 1-196 «VMN>
A; Residues: 1-196 «VMN>
A; Portetelle, D.; Hilger, F.
B; Wandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
B; Wandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
A; Woote: the nucleotide sequence Database, September 1995
A; Reference number: S56835
A; Reference number: S56835
A; Residues: 1-196 «VAM»
A; Rocasion: S57008
A; Woolecule type: DNA
A; Cross-references: EMBL: Z49493; NID:g1015607; PIDN: CAA89515.1; PID:g1015608; GSPDB:GNOC
C; Genetics:
A; Gene : MIPS: YJL218w
A; Cross-references: SGD:S0003754
A; Cross-references: SGD:S0003754
A; Cross-references: SGD:S0003754
A; Map Position: 10L
C; Superfamily: galactoside acetyltransferase
C; Keywords: acyltransferase
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: H88639
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
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Pred. No. 65;
0; Mismatches
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Ajcross-references: UNIPROT:021093; EMBL:275543; PIDN:CAA99870.1; GSPDB:GN00023; CESP:Ki
AjExperimental source: clone K01D12
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-393 < DUZ>
A;Residues: 1-393 < DUZ>
A;Cross-references: UNIPROT:O44163; EMBL:AF036694; PIDN:AAB88347.1; GSPDB:GN00022; CESP:A;Experimental source: strain Bristol N2; clone CD4
                                                                                                                                                                                                     A;Cross-references: UNIPROT:045144; GB:chr_IV; PIDN:AAC04390.1; PID:g2911817; GSPDB:GN00 C;Genetics:
A;Gene: C34H4.1
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wnstl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
A;Note: published_errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23181
R;Dobson, R
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T32533
R;Du, Z.; Scheet, P. Data Library, December 1997
A;Description: The sequence of C. elegans cosmid CD4,
A;Reference number: Z21185
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A;Introns: 152/2
C;Superfamily: Caenorhabditis elegans hypothetical protein K01D12.2
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A;Introns: 21/2; 71/2; 100/1; 195/3; 209/3; 319/2; 379/1
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A;Molecule type: DNA
A;Residues: 1-529 <WIL>
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Pred. No. 66;
1; Mismatches
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Length

DB 2;

Best Local Similarity 85.7%; Pred. No. 1e+02; Matches 6; Conservative 1; Mismatches 0; Indels

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2 STTTNYT 8 ||||:|| 478 STTTHYT 484

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Search completed: March 18, 2005, 19:11:05 Job time : 19.68 secs

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                                                                                                                                                                                                                                                                                                                                                        human
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Q717t5
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     GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                         1612378 segs, 512079187 residues
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ENV, HV1A2
O96668
Q81TW8
Q9YP43
Q9YP43
Q9YP43
Q9YP46
Q9YP48
Q9YP48
Q8KQ11
Q8KQ11
Q8KQ11
Q8KQ18
Q26933
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Q217D7
Q91CG
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Maximum Match 100%
Listing first 45 summaries
                            protein search, using sw model
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Q8JKL0
Q08732
Q6ZIX6
Q6QWE0
Q89M41
Q89M1
Q6DDT9
Q9DDT9
Q9BGPS
Q9BGPS
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Gapop 10.0 , Gapext 0.5
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2: uniprot_trembl:*
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21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-1986 (Rel. 44, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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          Q985n8
Q7rd05
Q45820
Q813r2
Q61m0
P251m0
P251m0
Q41575
Q09550
Q86163
Q16302
P40892
 Q842b3
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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Last annotation update)
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 Q842B3
Q985N8
Q7RD05
Q45820
Q813R2
Q6F1M0
PUPA PSEPU
Q41575
Q80163
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O15620
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01-NOV-1996 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
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ENV 4V1A2
LD - ENV 4V1A2
AC P03378; 19 - 1-01L-1986
DT 21-01L-1986
DT 05-01L-2004
DE ENVELOPE PO
DE GNYCOPTOCHER
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Gaps

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PERCENCE FROM N.A.

RODINSON-Rechavi M., Maina C.V., Gissendanner C., Laudet V.,

Robinson-Rechavi M., Maina C.V., Gissendanner C., Laudet V.,

B. Sluder A.B.;

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

B. Schoolson AAK17980.1;

R. GO, GO.000534;

R. GO, GO.000370;

R. Stranscription factor activity; IEA.

GO, GO.000370;

R. Transcription factor activity; IEA.

GO, GO.000370;

R. GO, GO.000356;

R. HARD receptor activity; IEA.

R. GO, GO.000356;

R. HARD receptor activity; IEA.

R. GO, GO.000356;

R. HARD receptor activity; IEA.

R. GO, GO.000356;

R. HARD receptor.

R. MART; SMO430;

R. RECEPTOR.

R. RECEPTO
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25-OCT-2004 (TTEMBLrel. 28, Last annotation update)
Nuclear hormone receptor family protein 80, isoform a (Nuclear ceceptor NRR-80).
Name=nhr-80; ORFNames=H10E21.3;
Caenorhabditis elegans.
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nuclear receptor NHR-80 (Fragment).
Caenorhabditis elegans.
Eukaryota; Matazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
815 815 N-linked (GlcNAc. . .) (Potential).
855 AA; 97438 MW; A3BC20573AAC41A2 CRC64;
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MEDLINE=99069613; PubMed=9851916;
Wormbase Consortium;
"Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
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Last annotation update)
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                                                                             Score 41; DB 1;
Pred. No. 8.4;
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01-07UN-2001 (TrEMBLrel. 17, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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PIR; A03976; VCLUA2.
HSSP; P04578; 1DLB.
HIV; K02007; ENV$SPE:
InterPro; IPR011010; DNA brk join_enz.
InterPro; IPR00077; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
Pfam; PF00517; GP41; 1.
                                                                                                                                MEDIJINE-85090453; PubMed-2578227; Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S., Stempien M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A., Levy J.A., Dina D., Luciw P.A.;
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        Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus. VCBI_TaxID=11685;
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- 1- SUBCELLULAR LOCATION, Nuclear (By similarity).
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- 1- SIMILARITY: Belongs to the nuclear hormone receptor family.
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- 1- SIMILARITY: Belongs to the nuclear hormone receptor activity; IEA.
- 1- SIMILARITY: Belongs in the nuclear hormone receptor activity; IEA.
- 20: GO:0003700; F:steroid hormone receptor activity; IEA.
- 30: GO:0003700; F:steroid hormone receptor activity; IEA.
- 30: GO:000350; F:steroid hormone receptor.
- 30: GO:000355; F:mon receptor.
- 30: GO:000355; F:mo
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SWART; SMO0430; HOLL; 1.
SMART; SMO0399; ZnF C4; 1.
DNA-binding; Metal-Binding; Nuclear protein; Receptor; Transcription;
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MEDLINE=21535983; PubMed=11679152; DOI=10.1089/088922201753197060;
Fang G., Burger H., Chappey C., Rowland-Jones S., Visosky A.,
Chen C.H., Moran T., Townsend L., Murray M., Weiser B.;
"Analysis of transition from long-term nonprogressive to progressive infection identifies sequences that may attenuate HIV type 1.";
                                                             "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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Davidson S., Wohldmann P., Courtney L.;
"The sequence of C. elegans fosmid H10E21.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
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Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transcription regulation; Zinc; Zinc-finger.
SEQUENCE 504 AA; 57345 MW; 06B95A963B4E0BB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Envelope polyprotein.

Human immunodeficiency virus 1.

Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
        MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 ASTTTNYS 191
                                         WormBase Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ASTTTNYT 8
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Bristol N2;
                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                         Waterston R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9YP43;
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Normpep; H10E21.3a; CE28733.

R GO; GO:0003707; F:steroid hormone receptor activity; IEA.

GO; GO:000335; Hrmon recept_1ig.

InterPro; IPR000345; Hrmon recept_lig.

InterPro; IPR000345; VitD_receptor.

InterPro; IPR001629; Znr Cd; receptor.

InterPro; IPR001629; Znf Cd; I.

R Ffam; PP00104; Hormone recep; 1.

R Ffam; PP00104; Hormone recep; 1.

R Ffam; PP00104; STR01DFINGER.

R FRINTS; PR00045; Znf Cd; I.

R PRINTS; PR00035; Znf Cd; I.

SWART; SM00430; HOLI; I.

SWART; SM00430; HOLI; I.

SWART; SM00430; Metal-Dinding; Nuclear protein; Receptor; Transcription; Transcription; Zinc; Zinc-finger.

SEQUENCE 486 AA; 55110 MW; 342484DD5C35BC64 CRC64;
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sluder A.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: Belongs to the nuclear hormone receptor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Robinson-Rechavi M., Maina C.V., Gissendanner C.R., Laudet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.2%; Score 37; DB 2; Length 486; 87.5%; Pred. No. 30;
                                                                                  STRAIN=Bristol N2;
Davidson S., Wohldmann P., Courtney L.;
"The sequence of C. elegans fosmid H10E21.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                Waterston R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Bristol N2; WormBase Consortium; Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Nuclear hormone receptor family protein 80, isoform b.
Name=nhr-80; ORFNames=H10E21.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          504 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AY204179; AAC82901.1; -.
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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166 ASTTTNYS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ASTITINY 8
                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P34021; 1R00
                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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HSSP;

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Q81748
Q81748
Q8177
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Q8177
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MEDINE-21535983; PubMed=11679152; DOI=10.1089/088922201753197060; Pang G., Burger H., Chappey C., Rowland-Jones S., Visosky A., Chen G.H., Marzay M., Weiser B.; Annier C.H., Warzar E.; Townsend L., Marray M., Weiser B.; Infection identifies sequences that may attenuate HIV type 1."; AIDS Res. Hum. Retroviruses 17:1395-1404(2001).

EMBL; U65986; ADLB.

HSSP; P04578; IDLB.
                                                                                                                                                                        MEDIJUBE-21535983; PubMed=11679152; DOI=10.1089/088922201753197060; Pang G., Burger H., Chappey C., Rowland-Jones S., Visosky A., Chen C.H., Moran T., Townsend L., Murray M., Weiser B.; "Analysis of transition from long-term nonprogressive to progressive infection identifies sequences that may attenuate HIV type 1."; AND TOS Res. Hum. Retroviruses 17:1395-1404 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    861 AA; 97993 MW; 3E3EFDC977CC18EA CRC64;
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:001901; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IFR000328; Env GP41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                 Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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57;
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100.0%; Pred. No. 58;
ative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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Best Local Similarity luv...
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
Envelope polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STTTNYT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P04578; 1DLB.
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                                                                                             NCBI_TaxID=11676;
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A Fang G., Burger H., Chappey C., Rowland-Jones S., Visosky A.,

Chen C.H., Moran T., Townsend L., Murray M., Weiser B.;

Tinfection identifies sequences that may attenuate HIV type 1.";

Infection identifies sequences that may attenuate HIV type 1.";

AIDS Res. Hum. Retroviruses 17:1395-1404(2001).

REMBL; U69585; AAD10883.1; -.

REMBL; U69585; AAD10883.1; -.

RO; GO:0019021; C:integral to membrane; IEA.

GO; GO:0019021; C:integral to membrane; IEA.

RO; GO:0019031; C:viral capsid; IEA.

RO; GO:0019031; C:viral envelope; IEA.

RO; GO:0019031; C:viral molecule activity; IEA.

RICHEPRO; IPRO00328; ENV GP41.
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                                                                                                                                                                                                                                                                                                                                                                                                          AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.2%; Score 37; DB 2; Length 860; 100.0%; Pred. No. 57; cive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 860 AA; 97738 MW; 1FEB24AAFD7F4216 CRC64;
                                                                                                         GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0051989; F:structural molecule activity; IEA.
InterPro; IPR000378; Env GP41.
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       Hum. Retroviruses 17:1395-1404(2001)
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Human immunodeficiency virus 1.
                                         EMBL; U69588; AAD10907.1; -. HSSP; P04578; IDLB.
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Matches 7; Conservative
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Pfam; PF00517; GP41; 1.
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KE Read T.D. Peterson S.N., Tourasse N.J., Bailie L.W., Paulsen I.T.,

Read T.D., Peterson S.N., Tourasse N.J., Essen J.A., Gill S.R.,

Nolson K.E., Tetrelin H., Foute D.E., Eisen J.A., Gill S.R.,

KOlonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,

A Kolonay J.F., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,

Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,

Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,

Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,

A Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,

A Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,

Hanna P.C., Kolstoe A.-B., Fraser C.M.;

The genome sequence of Bacillus anthracis Ames and comparison to
                                                                                                                                                                                                                                                MEDLINE=98037514; PubMed=9371463;
MEDLINE=98037514; PubMed=9371463;
MEDLINE=98037514; DubMed=9371463;
Maridon D., Daucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois Aldredge T., Bashizzadeh R., Blaely D., Cook R., Gilbert K., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Myani N., Carueo A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N., Complete genome sequence of Methanobacterium thermoautotrophicum deltali: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).
                                                                                                       Methanobacterium thermoautotrophicum.
Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
NCBI_TaxID=187420;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283 AA; 32015 MW; D89045B76AB76976 CRC64;
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01-UNN-2003 (TYEMBLrel. 24, Created)
01-UNN-2003 (TYEMBLrel. 24, Last sequence update)
25-OCT-2004 (TYEMBLrel. 28, Last annotation update)
Hypothetical protein.
OrderedLocusNames=BA2112, BAS1964, GBAA2112;
                           Last sequence update)
Last annotation update)
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Pred. No. 27;
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PIR, G69212, G69212.
InterPro, IPR002931, Trnsglumase_like.
        Created)
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SMART; SM00460; TGc; 1.
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      01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-JUN-2003 (TrEMBLrel. 24,
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                                                                                        OrderedLocusNames=MTH845;
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                                                                    Conserved protein.
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SEQUENCE 283 AA
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"Transcriptional and posttranscriptional control of cable pilus gene
expression in Burkholderia cenocepacia.";
J. Bacteriol. 186:1009-100(2004).
EMBL, AX114293; AAM56039.1;
SEQUENCE 900 AA; 96322 MW; D6FAFA1989E1392F CRC64;
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Microbiology 149:9871(2003).
EMBL, AY082893; AAL92875.1; -. SEQUENCE 900 AA; 96416 MW; AEC437197365C2D9 CRC64;
                                                                                                                                                                                                                                                                      Burkholderia cepacia (Pseudomonas cepacia).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
NCBI_TaxID=292;
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Burkholderiaceae; Burkholderia.
NCBI_TaxID=292;
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                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=14761995; DOI=10.1128/JB.186.4.1009-1020.2004;
                                                                                                                                                                 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Putative outer membrane usher.
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tive 0; Mismatches
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hes 7; Conservative
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Name=cblC;
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Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B., Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
Fraser C.M.;
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                                                                                                            Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K., Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R., Richardson P., Rubin B., Tice H.;
Submitted (JAN.2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AE017030, AAP25996.1;
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Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                            85.4%; Score 35; DB 2; Length 212; 87.5%; Pred. No. 31; 1.1 Indels iive 0; Mismatches 1; Indels
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Complete protecome; Hydrolase; Plasmid; Protease.
SEQUENCE 551 AA; 57726 MW; DC5907F6F027D056 CRC64;
                                             "Bacillus anthracis comparative genomics.";
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                       Complete proteome, Hypothetical protein.
SEQUENCE 212 AA; 24724 MW; F557E29021107126 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO: 0005509; F:calcium ion binding; IEA.
GO; GO: 0008237; F:metallopeptidase activity; IEA.
GO; GO: 0008237; F:metallopeptidase activity; IEA.
GO; GO: 0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001343; Hemlysn.Ca bind.
InterPro; IPR001818; Pept MINA_MIZB.
InterPro; IPR011049; Serralysn like_C.
Pfam; PP00353; HemolysinCabind; 6.
Pfam; PP00413; Peptidase MIO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
possible procease (EC 3.4.24.40).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORFNames=SMa0034;
Rhizobium meliloti (Sinorhizobium meliloti).
                                                                                                                                                                                                                                                                                                                                                                                                                                   551 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                       EMBL; AE017334; AAT31230.1; -. EMBL; AE017225; AAT54278.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00313; CABNDNGRPT.
SMART; SM00235; ZnMc; 1.
                                                                                                                                                                                                                                                                                              Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR, H95263, H95263.
HSSP, O69771, 10M8.
                                                                                                                                                                                                                                                                                                                                                              49 ASTTKNYT 56
                                                                                                                                                                                                                                                                                                                                      1 ASTTTNYT 8
                                                                                                                                                                                                                             GBAA2112; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM N.A.
                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid pSymA.
                                                                                                         STRAIN-Sterne;
                                                                                                                                                                                                                  BA2112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROSTRAIN=1021
                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                      Q931C8;
Q931C8;
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
Q931CB
ID Q931C
                                                                                                                                                                                                                   TIGR;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                 Epstein-Barr virus (strain B95-8) (HHV-4) (Human herpesvirus 4). Viruses, dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Lymphocryptovirus.
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Length 551
                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; F43043; QQBE34.
InterPro; IPR003840; Herpes helicase.
Pfam; PF02689; Herpes Helicase; 1.
ATP-binding; DNA replication; Early protein; Helicase.
APP-binding; DNA replication; Early protein; Helicase.
APP BIND 72 79
AEP BIND 72 809 AA; 89853 MW; 434AAA6EDAC01CC50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.4%; Score 35; DB 1; I
87.5%; Pred. No. 1.4e+02;
  DB 2;
                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Probable helicase.
Score 35; DB 2 Pred. No. 91; 0; Mismatches
                                                                                                                                                                                                                    809 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                    PRT;
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      85.4%;
87.5%;
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    Query Match
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          652 ASTTENYT 659
                                                                                                                        178 ASTTTGYT 185
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                                                                                 1 ASTTTNYT
                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10377;
                                                                                                                                                                                                                                                                                                                                         Name=BBLF4;
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                                                                                                                                                                                                                        HELI EBV P03214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                      RESULT 15
                                                                                                                                                                                                        HELI_EBV
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March 18, 2005, 18:51:00 ; Search time 161.84 Seconds (without alignments) 40.626 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                            - protein search, using sw model
                                                                                          OM protein
                                                                                                                                         Run on:
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BLOSUM62 Gapop 10.0 , Gapext 0.5 1 FERDISNVPFSPDGKPC 17 US-10-773-274A-2 97 Title: Perfect score: Scoring table: Sequence:

Total number of hits satisfying chosen parameters:

2105692 segs, 386760381 residues

Searched:

2105692

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_16Dec04:\*
1: geneseqp1980s:\*
2: geneseqp1990s:\*
3: geneseqp2000s:\*
4: geneseqp2001s:\* geneseqp20028:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp20048:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

		dŧ				
Result No.	Score	Query Match	Query Match Length DB	DB	ΙD	Description
1	97	100.0	1255	8	ADI95327	Adi95327 OSPF-rela
7	55	56.7	332	7	ABR63121	
m	52	56.7	332	۵	ADP84784	
4	55	56.7	332	æ	ADP84795	
ស	55	56.7	350	~	AAW27063	
9	51	52.6	846	7	ADB70258	
7	20	51.5	655	œ	ADS41636	Bac
ω	20		1136	æ	ADS30013	Ads30013 Bacterial
σ	48	49.5	1155	۵	ADS30836	Ads30836 Bacterial
10	47.5	49.0	669	ω	ADS23978	
11	47	48.5	134	ო	AAY75490	Aay75490 Neisseria
12	47	48.5	256	7	ABO65040	
13	47	48.5	590	9	ADB12353	Adb12353 Alloiococ
14	47	48.5	290	œ	ADJ27161	Adj27161 Alloiococ
15	47	48.5	626	æ	ADS41817	7
16	47	48.5	642	7	AAY01541	Aay01541 Alpha(2-3
17	46	47.4	120	Ŋ	ADH32823	m
18	46	47.4	508	8	ADN26478	Adn26478 Bacterial
19	46	47.4	613	œ	ADS22148	Ads22148 Bacterial
20	46	47.4	756	œ	ADS30912	Ads30912 Bacterial
21	45	46.4	207	œ	ADN23184	Adn23184 Bacterial
22	45	46.4	275	œ	ADS88240	Ads88240 Human pro
23	45	46.4	288	~	AAR22996	Aar22996 Yeast pro
24	45	46.4	288	4	ABG09463	
25	45	46.4	288	9	ABR53144	Abr53144 Protein s

Adk63118 Disease t Ad844003 Bacterial Adh78730 Tobacco A			ADO84991 Human can Adj78138 Peptide S Abg96085 Cysteine-	Aao04124 Human pol Abp06586 Human ORF Aay73870 Human pro		Abr53208 Protein s Adk63748 Disease t Adn19303 Bacterial Adn18891 Bacterial
ADK63118 ADS44003 ADH78730	ABG09464 ADS29812 AAG43935	AAM25263 ABO84990	ABC84391 ADJ78138 ABG96085	AAO04124 ABP06586 AAY73870	ADN24340 ABO72047	ABK53208 ADK63748 ADN19303 ADN18891
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288 288 377	596 1118 117	414	451 27 29	108 167 210	395	594 594 613 613
46.4 46.4 46.4	46.4	0.00	4 4 4 5 5 7 7 4 4	4 4 5	4.4.	4.4.4.4.
4 4 4	4 4 4	4 4 4	4 4	4 4 4	4 4	4 4 4 4
4 4 4 R R R	44 45 5 5	444.5	4 4 4 4 4 4	4 4 4 4 4 4	44.	ਧਾ ਧਾ ਧਾ ਧਾ ਧਾ ਧਾ
26 27 28	3 3 3 3 3 3 4 3 5 5 5 5 5 5 5 5 5 5 5 5	2000	# 55 W 10 W 10 W 10 W 10 W 10 W 10 W 10 W 10	337 398	410	4 4 4 4 2 6 4 6

# ALIGNMENTS

immune response; overlapping synthetic peptide formulation; OSPF; immunostimulant; virucide; antibacterial; antiparasitic; cytostatic; vaccine; viral; bacterial; parasitic infection; prion disease; OSPF-related SARS coronavirus Frankfurt 1 spike protein S. ADI95327 standard; protein; 1255 AA SARS coronavirus Frankfurt 1. 27-JUN-2003; 2003WO-US020322. 27-JUN-2002; 2002US-0392718P. (first entry) neoplastic; toxin; spike. WO2004002415-A2 08-JAN-2004. 04-NOV-2004 ADI95327; RESULT 1 ADI95327 

(DAND ) DANA FARBER CANCER INST INC.

ŝ Ruprecht RM, Jiang

WPI; 2004-082868/08.

Modulating an immune response, useful for treating immune disorders, e.g. viral, bacterial and parasitic infections, prion diseases, or neoplastic diseases, administering to a subject an overlapping synthetic peptide formulation.

Claim 13; SEQ ID NO 235; 175pp; English.

The invention relates to a novel method for modulating an immune response comprising administering to a subject an overlapping synthetic peptide formulation (OSPF) which comprises a combination of single chain peptides corresponding to the amino acid sequence of a protein of interest. The method of the invention has immunostimulant, virucide, antibacterial, antiparasitic and cytostatic applications and may be useful during vaccine production and for treating immune disorders including viral, bacterial and parasitic infections, prion diseases, neoplastic diseases, as well as providing protection against toxins. The current sequence is that of the OSPF-related SARS coronavirus Frankfurt 1 spike protein S of

Query Match

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Novel variant of parent glycoside hydrolase family 53 galactanase, useful in dairy industry, to prepare galacto-oligosaccharide and/or for hydrolysis of lactose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glycoside hydrolase family 53 galactanase; GH family 53 galactanase; dairy industry; galacto-oligosaccharide preparation; lactose hydrolysis; enzyme; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention comprises variants of a glycoside hydrolase (GH) family 53 galactanase. The GH family 53 galactanase variants of the invention are useful in the dairy industry for the preparation of galactooligosaccharide and the hydrolysis of lactose. The present amino acid sequence represents a wild type Corynascus heterothallicus GH family 53
                                                           aide hydrolase family 53 galactanase; GH family 53 galactanase; industry; galacto-oligosaccharide preparation; lactose hydrolysis;
                          Corynascus heterothallicus glycoside hydrolase family 53 galactanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mutant C. heterothallicus glycoside hydrolase family 53 galactanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 55; DB 8; Length 332; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                         Christensen LLH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "Wild type Ala replaced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                                                                                            Borchert TV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 19; SEQ ID NO 1; 262pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADP84795 standard; protein; 332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     galactanase of the invention
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259 FPSDVKNIPFSPEGQ 273
                                                                                                                                                                                                                                      11-DEC-2003; 2003WO-DK000851.
                                                                                                                                                                                                                                                                          20-DEC-2002; 2002DK-00001968.
08-APR-2003; 2003DK-00000537.
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                                                                                                                                    Corynascus heterothallicus.
(first entry)
                                                                                                                                                                                                                                                                                                                                                              Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                          (NOVO ) NOVOZYMES AS
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                        WO2004056988-A2.
                                                                                                                                                                                                                                                                                                                                                                           Ryttersgaard C;
 23-SEP-2004
                                                                                                                                                                                                                                                                                                                                                              De Maria L,
                                                                                                                                                                                                          08-JUL-2004
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                                                                   glycoside
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                                                                                     dairy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the protein sequence of a thermostable galactanase (without the signal peptide) of Myceliophthora thermophila. Preferred variants of the galactanase can be used in a claimed composition of the invention, which comprises at least 2 thermostable enzymes selected from an endoglucanase, xylanase, phytase, protease, galactanase, marmanase and alpha-galactosidase. The composition is useful for improving the nutritional value of animal feeds, especially those containing soya, wheat, barley, oats and/or rye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Composition useful as an animal feed additive comprises at least two thermostable enzymes selected from endoglucanase, xylanase, phytase, protease, galactanase, mannanase, dextranase and alpha-galactosidase
                                                                                                           Gaps
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0
                                                                       100.0%; Score 97; DB 8; Length 1255; 100.0%; Pred. No. 7e-07;
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                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                      Galactanase; thermostable; enzyme; feed additive.
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                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                     Myceliophthora thermophila galactanase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADP84784 standard; protein; 332 AA.
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FPSDVKNIPFSPEGQ 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JAN-2002; 2002DK-00000130
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Myceliophthora thermophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HOFF ) ROCHE VITAMINS AG.
                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                              17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pettersson D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-731382/69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                         Best Local Similarity Matches 17; Conserv
                                            Sequence 1255 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003062409-A2
        the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-JUL-2003.
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                                                                                                                                                                                                                                                                                                       ABR63121;
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Gaps

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3; Indels

/note= "Wild type His replaced by Asp"

ADP84784

XXX

RESULT 3 ADP84784

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ŝ Larsen Muellertz A;

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This protein comprises Myceliophthora thermophila galactanase (EC-
3.2.1.89), as encoded by a cDNA clone (see AAT85058) insert in plasmid
pVES 2.0, present in Saccharomyces cerevisiae DSM 9983. The galactanase
catalyses the endohydrolysis of 1,4-beta-D-galactosidic linkages in
arabinogalactans. It has a pH optimum of 6.0, a mol.wt. of 42 kba, a pI
of 7.8, a temperature optimum of 70 deg C, and a Km (* galactan) of 0.5-
0.9. The galactanase is useful in methods for the preparation of feed or
food, for reducing the viscosity or water binding capacity of a plant
wall-derived material, and in the production of wine or fruit or
vegetable juice, especially the depectinisation of apple and pear juice.
It can be expressed in transformed host cells and isolated in pure form,
free of contaminating enzyme activities. 2 Motifs (see AAW27065-66) that
are also found in Humicola insolens galactanase (see AAW27065) can be
cused to design primers (see AAT85060-61) useful in the isolation of
galactanases from other fungl of the order Sordariales. (Updated on 25-
MAR-2003 to correct PI field.) (Updated on 17-OCT-2003 to standardise OS
                                                                                                                                                                                                                             Fungal galactanase and related DNA - useful in animal feed industry and fruit juice depectinisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.7%; Score 55; DB 2; Length 350; 53.3%; Pred. No. 1.8; 3; Indels iive 4; Mismatches 3; Indels
                                                                                                                                  Kofod LV, Kauppinen MS, Andersen LN, Clausen IG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C. neoformans amino acid sequence SEQ ID NO:3302.
                                                                                                                                                                                                                                                                                         Claim 23; Page 47-48; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB70258 standard; protein; 846 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fungicide; gene therapy; infection
97WO-DK000092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-DEC-2001; 2001US-0341261P.
                                      96DK-00000233
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277 FPSDVKNIPFSPEGQ 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FERDISNVPFSPDGK 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eroshkin AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cryptococcus neoformans
                                                                                              (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-448686/41.
N-PSDB; AAT85058.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 350 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003052076-A2.
28-FEB-1997;
                                    01-MAR-1996;
                                                      01-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB70258;
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                                                                                                                                                                                                                                                                                                   Novel variant of parent glycoside hydrolase family 53 galactanase, useful
in dairy industry, to prepare galacto-oligosaccharide and/or for
hydrolysis of lactose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Galactanase, fruit juice, vegetable juice, wine, pectin, depectinisation,
animal feed, foodstuff.
                                                                                                                                                                                                                                                                                                                                                                                                                     The invention comprises variants of a glycoside hydrolase (GH) family 53 galactanase. The GH family 53 galactanase variants of the invention are useful in the dairy industry for the preparation of galacto-oligosaccharide and the hydrolysis of lactose. The present amino acid sequence represents a mutant Corynascus heterothallicus GH family 53 galactanase of the invention. NOTE: The present sequence is not shown in the specification, but has been created using the wild type Corynascus heterothallicus GH family 53 galactanase ADP84784 as a template.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                               Christensen LLH, Larsen S;
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53.3%; Pred. No. 1.7;
ive 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynascus heterothallicus; strain CBS 117.65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Myceliophthora thermophila galactanase.
                                                                                                                                                                                                             Borchert TV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19. .350
/label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .18
/label=_Sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Claim 7"
                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page; 262pp; English
                                                                          11-DEC-2003; 2003WO-DK000851
                                                                                                              20-DEC-2002; 2002DK-00001968.08-APR-2003; 2003DK-00000537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 FPSDVKNIPFSPEGQ 273
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 56.7
Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                               Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
                                                                                                                                                                                                                                                                       WPI; 2004-507720/48.
                                                                                                                                                                      (NOVO ) NOVOZYMES
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WO2004056988-A2.
                                                                                                                                                                                                                                 Ryttersgaard C;
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25-MAR-2003
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                                    08-JUL-2004
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RESULT 5

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AAW27063
IID AAW3
ACC AAW2
XXX AAW2
XXX II7-C
DDT 28-E
DD

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Gaps

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WPI; 2004-061375/06
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Matches 8; Conserv
                                                                                                                                                                                                                                                                            Sequence 655 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ADS30013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria.
                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SLAT/)
(CHEN/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HINK/)
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                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
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8,49,69,99,99,99,99,99,99,99,99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                        The invention relates to a novel purified or isolated Cryptococcus neoformans nucleic acid molecule comprising a sequence encoding a polypeptide comprising a sequence not given in the specification. A polynucleotide of the invention has fungicide activity, and may have a use in gene therapy. The nucleic acid is useful for preparing a composition for treating an infection caused by Cryptococcus neoformans. The present sequence represents a C. neoformans sequence of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                                                             Gaps
                     useful for preparing a composition for treating an
                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                      52.6%; Score 51; DB 7; Length 846; 60.0%; Pred. No. 24;
                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goldman BS;
                                 infection caused by Cryptococcus neoformans
                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 20066; 122pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen X,
                                                    Claim 9; SEQ ID NO 3302; 136pp; English
                                                                                                                                                                                                                                                                                                                                               ADS41636 standard; protein; 655 AA
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FKRKVHHVSFSPDGK 109
                                                                                                                                                                                                                                                                                                                                                                                                             Bacterial polypeptide #20066
                                                                                                                                                                                                                                                                   1 FERDISNVPFSPDGK 15
                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                               9; Conservative
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HINKLE G J.
SLATER S C.
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                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hinkle GJ,
                     nucleic acid,
 N-PSDB; ADB69175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2003233675-A1.
                                                                                                                                                                                                   Sequence 846 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HINK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (COLD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHEN/)
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                                                                                                                                                                                                                                               Matches
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polymucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant the crombinant DNA construct and growing the transformed plant with the recombinant DNA construct and growing the transformed plant, where the polymucleotide or polypeptide is useful for improving plant with the crecombinant DNA construct is useful for improving plants with construct or insproved plant properties, e.g. improved cold, heat or drought tolerance, improved plant properties, e.g. improved cold, heat or drought tolerance, concreased resistence to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan condition in the printed specification but was obtained in 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
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Pred. No. 26;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.5%; Score 50; 53.3%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12
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SLATER S C.
CHEN X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GOLDMAN B S.
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to prowide for expression of a polymoclectide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant combinant DNA construct and growing the transformed plant, where the polymuclectide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for producing plant properties. The recombinant plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osemotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved vield by modification of carbohydrate, nitrogen or providing improved vield by modification of carbohydrate, nitrogen or providing improved vield by modification of carbohydrate, nitrogen or provided when the properties of the coll or uptake, by modification of photopynthesis or by
                   New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.5%; Score 50; DB 8; Length 1136; 64.3%; Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                  Claim 1; SEQ ID NO 19046; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADS30836 standard; protein; 1155 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacterial polypeptide #19869.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-FEB-2003; 2003US-00369493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-FEB-2002; 2002US-0360039P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :::|| |||||
| 648 EQTVNNVYFSPDGK 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 ERDISNVPPSPDGK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-DEC-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2003233675-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADS30836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
ADS30836
8
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(CAOY/) CAO Y. (HINK/) HINKLE G J.

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promoter functional in a plate cell, where the promoter is positioned to promoter functional in a plate cell, where the promoter is positioned to promoter functional in a polymucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property comprises transformed plant with the combinant DNA construct comprises transformed plant where the polymucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with the improved plant properties, e.g. improved cold, heat or drought tolerance, colerance to herbicides, extreme osmotic conditions, pathogens or peets, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, introgen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved plants production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form at from them intend the data of the form of the form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                      New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance, drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                              The invention relates to a recombinant DNA construct comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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57.1%; Pred. No. 1.1e+02;
tive 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Format from USPTO at segdata.uspto.gov/sequence.html
                                                                                                     Goldman BS;
                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 19869; 122pp; English.
                                                                                                     Chen X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADS23978 standard; protein; 699 AA.
                                                                                                   Slater SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacterial polypeptide #13011.
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1108 QRGVNSVSFSPDGK 1121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 57.13
Matches 8; Conservative
                                             GOLDMAN B S.
                                                                                                                                                   WPI; 2004-061375/06
SLATER S C.
                                                                                                   Hinkle GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1155 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2003233675-A1
                        CHEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADS23978;
(SLAT/)
(CHEN/)
                                                  (GOLD/)
                                                                                                Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADS23978
BXBXSXEEEEE
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Gaps

Masignani V, Mora M; Scalato E, Scarselli M;

CHEN X

CAOY/) HINK/)

(dolp) (SLAT/) (CHEN/)

Cao Y,

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Novel Neisserial polypeptides predicted to be useful antigens for
                                                                                                                                                                                                                                                                                                                                                                                                                                         Fraser C, Galeotti C, Grandi G, Hickey E,
Petersen J, Pizza M, Rappuoli R, Ratti G,
Tettelin H, Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 1173; 1453pp; English
                                                                                                                                                                 98US-0094869P.
98US-0099062P.
98US-0103749P.
98US-0103749P.
                                                                                             99WO-US009346
                                                                                                                                                                                                                                                                                                                          99US-0121528P
                                                                                                                                                                                                                                                                                                                                                                                                INST GENOMIC RES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US6610836-B1
                                                                                                                                                                                                                                                                      09-OCT-1998;
09-OCT-1998;
25-FEB-1999;
WO9957280-A2
                                                                                             30-APR-1999;
                                                                                                                                                                      31-JUL-1998;
02-SEP-1998;
                                              11-NOV-1999.
                                                                                                                                                 01-MAY-1998
                                                                                                                                                                                                                       02-SEP-1998
                                                                                                                                                                                                                                                    09-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                           (CHIR )
                                                                                                                                                                                                                                                                                                                                                                                                  (GENO-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABO65040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to promote functional in a plant cell, where the promoter is positioned to promote for expression of a polynucleotide encoding a polypoptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property comprises transforming a plant with the the avoing an improved property comprises transforming a plant with the combinant DNA construct and growing the transformed plant, where the copy oblynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plant properties. The recombinant DNA construct is useful for producing plant with the improved plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to harbicides, extreme osmociac conditions as pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modification of carbohydrate, nitrogen or content, improved lignin production of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved lignin production of migroved galactomannan production. This sequence represents a bacterial polypeptide used in the condition, improved lignin production on improved galactomannan production. This sequence represents a bacterial polypeptide used in the format from terminal for when the form this patent did not format from improve the path of the printed specification of production in electronic format from improve the sequence data for this patent did not format from improve the sequence fate for this patent did not format from the printed precification of pathons and the sequence fate for this patent did not format from the printed for the
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                                                                                                                                                                                                                                                                                                                                                                           New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseria meningitidis ORF 727 protein sequence SEQ ID NO:2454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.0%; Score 47.5; DB 8; Length 699; 55.6%; Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           format from USPTO at seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                Goldman BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 73;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 13011; 122pp; English.
                                                                                                                                                                                                                                                                                Hinkle GJ, Slater SC, Chen X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY75490 standard; protein; 134 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ERDISNVPF---SPDGKP 16
                               20-FEB-2003; 2003US-00369493.
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137 QRDIKNYPFKVVNKDGKP
                                                                                21-FEB-2002; 2002US-0360039P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 55.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis
                                                                                                                               CAO Y.
HINKLE G J.
SLATER S C.
                                                                                                                                                                                                                               GOLDMAN B S.
                                                                                                                                                                                                                                                                                                                                    WPI; 2004-061375/06.
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represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54577 to AAZ54576 and AAZ5456 to AAZ54591 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54575 to AAZ54576 and AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisseria bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant expression vector; transcription regulatory element; Klebsiella pneumoniae protein; antibacterial; Vaccine.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klebsiella pneumoniae polypeptide segid 11557.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 12;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            48.5%; Score 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABO65040 standard; protein; 256 AA.
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99 ERDLCKIPFPPDSR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ERDISNVPFSPDGK 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 134 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-AUG-2003.
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AAY75490;

RESULT 11

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Alloiococcus otitidis genomics an abstract purpose an antigenic protein.
Alloiococcus otitidis is a Gram-positive bacterium. Also described: (1)
an isolated polypeptide that is encoded by the polymucleotide (1); (2) an expression vector comprising the novel isolated polymucleotide (1); (2) an expression vector comprising the novel isolated polymucleotide (1); its complement, degenerate variant or fragment; (3) a genetically engineered composition comprising the polypeptide of (1); (5) an immunogenic composition comprising the polypeptide of (1); (5) an immunogenic composition comprising the polypeptide of (1); (6) a pharmaceutical composition comprising the expression vector; (6) a pharmaceutical composition comprising the captive of (1) and a carrier; (7) a protein chip comprising an array of the polypeptide of (1) and a carrier; (7) a protein chip comprising the colypeptide of (1) and a carrier; (7) a protein comprising the colypeptide of (1), their biological equivalent or fragment; (8) immunogenic composition; (9) detecting and/or identifying Alloiococcus critidis in the biological sample; (10) a kit comprising a container containing the novel polymucleotide, its degenerate variant or fragment, or the antibody of (4); and (11) producing a polypeptide by culturing the colypeptide from the culture. (1) can be used in gene therapy. The colymucleotides, polympetides, antibodies and compositions of the present invention can be used for treating and diagnosing diseases, drug cinical trials. The polymucleotides are useful for expressing and detecting Alloiococcus otitidis antigen protein from the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alloiococcus otitidis protein, a novel antibacterial target SeqID 106.
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   present invention describes an isolated polynucleotide (I) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   growth and survival; otitis media with effusion; OME; bacterial infection; antibacterial; antiinfective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 6;
73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADJ27161 standard; protein; 590 AA.
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18-NOV-2002; 2002US-0426742P.
18-NOV-2002; 2002US-0427367P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 NVPFSPDGKPC 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2004-053616/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ADJ27160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 590 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003104391-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADJ27161;
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ADJ27161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for preparing a vaccine composition against Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oţ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alloiococcus otitidis; antigenic protein; immunogenic; immunisation; gene therapy; Gram-positive bacterium; infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Russell DP, Zagursky RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alloiococcus otitis antigenic protein SEQ ID NO:6360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 11557; 932pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                      (GENO-) GENOME THERAPEUTICS CORP.
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                                                                                     99US-0117747P.
                    27-JAN-2000; 2000US-00489039.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-NOV-2002; 2002WO-US036123
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                                                                                                                                                                                                                       Osborne M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2003-505284/47.
                                                                                                                                                                                                                                                                                    WPI; 2003-895346/82.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                         N-PSDB; ACH98591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 256 AA;
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                                                                                        29-JAN-1999;
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                                                                                                                                                                                                                       Breton GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB12353;
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This invention relates to novel isolated Alloiococcus otitidis (A. otitidis) nucleic acid molecules and encoded proteins thereof. Specifically, it refers to proteins that are essential for the growth and survival of the gram-positive bacterium A. otitidis, and hence provide novel antibacterial targets. The present invention describes pharmacutical compositions and antisense compounds that are useful for inhibiting activity or expression of these proteins. Furthermore, it provides diagnostics and therapeutics that can be used to ameliorate diseases that are associated with A. otitidis, such as otitis media with effusion (OME) and various bacterial infections. Accordingly, these compositions exhibit both antibacterial and antiinfective activities. This polypeptide is an A. otitidis protein sequence of the invention.
                        Claim 7; SEQ ID NO 106; 433pp; English
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Sequence 590 AA;

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48.5%; Score 47; DB 8; Length 590; 63.6%; Pred. No. 73;
                           2; Indels
                           Mismatches
                           2,
                            Conservative
                                                    7 NVPFSPDGKPC 17
                                                                           63 NCPYSDDGEPC 73
             Best Local Similarity
Matches 7; Conserv
  Query Match
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ADS41817 standard; protein; 626 AA.
                                                                                                                                        Bacterial polypeptide #20247.
                                                                                                       (first entry)
                                                                                                       02-DEC-2004
                                                                     ADS41817;
RESULT 15
                  ADS4181
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Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombinition; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide. 

Bacteria.

US2003233675-A1.

20-FEB-2003; 2003US-00369493 18-DEC-2003.

21-FEB-2002; 2002US-0360039P

CAO Y. HINKLE G J. SLATER S C. CHEN X (HINK/) (CHEN/) CAOY/)

GOLDMAN B S

Goldman BS; Chen X, Slater SC, Hinkle GJ, Cao Y,

WPI; 2004-061375/06.

The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to Claim 1; SEQ ID NO 20247; 122pp; English.

New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

provide for expression of a polymucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant combinant DNA construct and growing the transformed plant, where the recombinant DNA construct is useful for improving plant with the polymucleotide or polypeptide is useful for improving plant properties.

The recombinant DNA construct is useful for improving plants with improved plant properties, e.g. improved cold, heat or drought tolerance, improved plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the condition, increased resistance to plant disease, better growth rate by modification of the condition or plant growth and development under all and/or content, improved plant growth and development under at least one stress providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan condition, improved lignin production or improved galactomannan condition, improved lignin production or improved galactomannan condition, inthe sequence repersents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not confirm part of the printed specification but was obtained in electronic correct form part of the printed specification but was obtained in electronic correct form part of the printed specification but was obtained in electronic correct form part of the printed specification but was obtained in electronic correct form part of the printed specification but was obtained in electronic correct form part of the printed specification but was obtained to the correct form part of the printed proved form to the correct form part of the printed proved form to 

Sequence 626 AA;

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Gaps ö

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Search completed: March 18, 2005, 19:10:14 Job time : 165.84 secs

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Sequence 11557, A
Sequence 1157, A
Sequence 4, Appli
Sequence 14, Appli
Sequence 13, Appli
Sequence 18, Appl
Sequence 958, Appl
Sequence 764, Appl
Sequence 20793, A
Sequence 20793, A
Sequence 14113, A
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10450, A
2, Appli
4, Appli
27452, A
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                                                                          March 18, 2005, 18:59:50 ; Search time 41.48 Seconds (without alignments) 30.594 Million cell updates/sec
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Sequence 4
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/cgm2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgm2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgm2_6/ptodata/1/iaa/Re_COMB.pep:*
/cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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        GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
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US-09-039A-11557

US-09-99-039A-11557

US-09-955-909-4

US-09-902-540-14114

US-09-902-540-14114

US-09-538-092-958

US-09-538-092-958

US-09-538-092-958

US-09-522-991A-20793

US-09-922-938-13801

US-09-489-039A-13801

US-09-489-039A-13801

US-09-489-039A-13801

US-09-489-039A-13801

US-09-489-039A-14813

US-09-137-855-4

US-09-137-855-4

US-09-137-855-4

US-09-137-855-4

US-09-137-856-4

US-09-902-540-10450

US-09-362-336A-2

US-09-362-336A-2

US-09-362-336A-2

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Listing first 45 summaries
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                    Sequence 10614, A Sequence 15380, A Sequence 2, Appli Sequence 194, Appli Sequence 2828, A Sequence 7, Appli Sequence 7, Appli Sequence 1352, A Sequence 1352, A Sequence 17, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli
  Sequence 18853,
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US-09-137-855-2

Sequence 2, Application US/09137855B

PRIENT No. 6242237

GENERAL INFORMATION:

APPLICANT: Kauppinen, Markus S.

APPLICANT: Andersen, Lene N.

APPLICANT: Andersen, Lene N.

APPLICANT: Andersen, Lene N.

PAPLICANT: Andersen, Lene N.

PAPLICANT: Andersen, Lene N.

APPLICANT: Andersen, Lene N.

PAPLICANT: Andersen, Lene N.

APPLICANT: Andersen, Lene N.

EARLIER PILING DATE: 1998-08-21

EARLIER PILING DATE: 1996-03-01

EARLIER PILING DATE: 1996-03-01
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APPLICANT: Kofod, Lene
APPLICANT: Rauppinen, Markus
APPLICANT: Clausen, Lene
APPLICANT: Clausen, Lene
APPLICANT: Mullertz, Anette
TITLE OF INVENTION: An Enzyme With Galactanase Activity
FILE REFERENCE: 4686.514-US
CURRENT APPLICATION NUMBER: US/09/723,548C
                  US-09-902-540-10614

US-09-902-540-15380

US-08-311-731A-64

US-08-311-731A-64

US-08-311-731A-64

US-09-252-991A-28289

US-09-355-166-5

US-09-355-166-5

US-09-355-166-5

US-09-418-328-3

US-09-411-328-3

US-09-411-328-3

US-09-846-729A-1

US-09-846-729A-1

US-09-846-729A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.7%; Score 55; DB 3;
llarity 53.3%; Pred. No. 0.57;
Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) ORGANISM: Myceliophthora thermophila
US-09-137-855-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-723-548C-2
; Sequence 2, Application US/09723548C
; Patent No. 6485954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        277 FPSDVKNIPFSPEGQ 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FERDISNVPFSPDGK 15
Query Match
Best Local Similarity
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.5%; Score 47; DB 3; Length 642; 60.0%; Pred. No. 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
SOFTWARE: FastSEQ Version 2.0
SOFTWARE: FastSEQ Version 2.0
RAPLICATION NUMBER: US/09/955,909
FILING DATE: 18-Sep-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 08/911,393
FILING DATE: «Unknown»
ATTORNEY/AGNNT INFORMATION:
NAME: COTUZZI, LAULER A
REGISTRATION UNMBER: 30,712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                               TELING JATE: INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7188-032-999
TELEPHONE: (212) 7909090
TELEPHONE: (212) 869941
TELEFA: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 642 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: PELLETIER, Marc
BARKER, William A.
HAKES, David J.
ZOPF, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09955909
Patent No. 6706497
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212)7909090
TELEFAX: (212)8699741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 642 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FERDISNVPFSPDGK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 FKRQSSKVPFEKDGK 26
                                                                                                                                                                                                                                                                                                                                  LENGTH: 642 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local, Similarity 60.03
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: PINEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF EXQ ID NOS: 14342
ENG THE SEQ ID NOS: 14342
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APPLICANT: BARKER, William A.
APPLICANT: BARKER, William A.
APPLICANT: AFEC, David A.
TITLE OF INVENTION: METHODS FOR PRODUCING
TITLE OF INVENTION: SIALYLOLIGOSACCHARIDES IN A DAIRY SOURCE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.5%; Score 47; DB 4; Length 256; 52.9%; Pred. No. 8; tive 2; Mismatches 6; Indels
                                                                                                                                                                                                  Query Match
56.7%; Score 55; DB 4; Length 350;
Best Local Similarity 53.3%; Pred. No. 0.57;
Matches 8; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11557, Application US/09489039A Patent No. 6610836 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FRAESEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,393
                                                                                                                  ; TYPE: PRT
; ORGANISM: Myceliophthora thermophila
US-09-723-548C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08911393
Patent No. 6323008
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 2
LENGTH: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :| ||| || :| ||
127 YELIISNPPFFAEGVPC 143
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IBM Compatible
                                                                                                                                                                                                                                                                                                                         277 FPSDVKNIPFSPEGQ 291
                                                                                                                                                                                                                                                                                                  1 FERDISNVPFSPDGK 15
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Best Local Similarity 52.9
Matches 9; Conservative
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COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-489-039A-11557
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US-08-911-393-4
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Gaps
                                                                                                                                                                                                         APPLICANT: Hlavka, Joseph J.
APPLICANT: Pincus Matthew R.
APPLICANT: Pincus Matthew R.
APPLICANT: No. 58406831e, John F.
APPLICANT: Abajian, Henry B.
APPLICANT: Kende, Andrew S.
TITLE OF INVENTION: Peptides Inhibiting the Oncogenic Action TITLE OF INVENTION: of P21 Ras
NUMBER OF SEQUENCES: 5.2
CORRESPONDENCE ADDRESS:
ADDRESSER: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,525
FILING DATE: 21-SEP-1995
CLASSIFICATION: 530
ATTONREY/AGENT INPOME/ATTON:
NAME: REFERENCE/DORGET UNMBER: 33,878
REGISTRATION NUMBER: 33,878
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hlavka, Joseph J.
APPLICANT: Pincus, Matchew R.
APPLICANT: No. 59104781e, John F.
APPLICANT: Abajian, Henry B.
APPLICANT: Kende, Andrew S.
APPLICANT: Kende, Peptidomimetics Inhibiting
TITLE OF INVENTION: the Oncogenic Action of P21 Ras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45; DB 2;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: Caenorhabditis elegans
US-08-531-525-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-718-270A-48
; Sequence 48, Application US/08718270A
; Patent No. 5910478
; GENERAL INFORMATION:
                                                                                                                       US-08-531-525-48
Sequence 48, Application US/08531525
Patent No. 5840683
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
                  | :| | : :||||:
38 FSKDYSEIHYSPDGR 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 204 amino acide
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 PFKDDGKPC 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
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APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
TITLE OF INVENTION: OTHER CONDITIONS
FILE REFERENCE: 1279-338G3/0980138
CURRENT APPLICATION NUMBER: US/09/460,2958
CURRENT APPLICATION NUMBER: US 09/163,047
PRIOR PILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE PATENTIN VERSION 3.1
SEQ ID NO 13
LENGTH: 571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: 2001-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 14114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                Query Match
Best Local Similarity 60.0%; Pred. No. 23;
Matches 9; Conservative 1; Mismatches 5; Indels
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Pred. No. 29;
4; Mismatches 4; Indels
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Pred. No. 6.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                         US-09-902-540-14114
; Sequence 14114, Application US/09902540
; Patent No. 6833447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13, Application US/09460295B
Patent No. 6710030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 57.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                       1 FERDISNVPFSPDGK 15
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109 YEPDVEGVAFSPDG 122
                                                                                                                                                                                                                                                                                                  12 PKROSSKVPFEKDGK 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-14114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; URGANISM: Bothrops jararaca
US-09-460-295B-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FERDISNVPFSPDG 14
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Best Local Similarity 46.7%
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US-09-460-295B-13
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1 FERDISNVPFSPDGK 15

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Sequence 20793, Application US/09252991A

Sequence 20793, Application US/09252991A

Sequence 20793, Application US/09252991A

GENERAL INFORMATION:
THE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REPREMENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PLING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

SEQ ID NO 20793

SEQ ID NO 20793

LENGTH: 548
                                                                                                                                                                                                                                                                                                                                                           | Sequence 764 Application US/09538092
| Sequence 764 Application US/09538092
| Patent No. 6753314
| GENERAL INFORMATION:
| APPLICANT: Giot, Loic
| APPLICANT: Mansfield, Traci A.
| TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
| FILE REFRENCE: 15966-54
| CURRENT APPLICATION NUMBER: US/09/538,092
| CURRENT APPLICATION NUMBER: 60/127,352
| PRIOR APPLICATION NUMBER: 60/127,352
| PRIOR APPLICATION NUMBER: 60/127,352
| PRIOR FILING DATE: 2000-02-01
| PRIOR FILING DATE: 2000-02-01
| NUMBER OF SEQ ID NOS: 1387
| SEQ ID NO 764
| LENGTH: 288
                                                                                                                                                           Gaps
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                                                                                                      Score 45; DB 4; Length 275;
Pred. No. 18;
3; Mismatches 5; Indel8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YOR362C
US-09-538-092-764
; DB 4;
; 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                             Query Match 46.4%; Score 45; Best Local Similarity 46.7%; Pred. No. 3 Matches 7; Conservative 3; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.4%; Score 45; 66.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20793
                                                                                                                                                                                                                                           : | | |: |:|||
212 DEDESQAPYDPNGKP 226
                                                                                                                                                                                                              2 ERDISNVPFSPDGKP 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 66.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                              RESULT 11
US-09-538-092-764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
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; Sequence 958. Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFRENCE: 15966-54
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 2000-02-01
; PRIOR FILING DATE: 2000-02-01
; SOFTWARE: CurapatSeqFormatter Version 0.9
; SEQ ID NO 958
; LANGTH: 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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Pred. No. 13;
0; Mismatches 2; Indels
                                                                                                                                                                                   CZIP: 80303

CZIP: 80304

MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC compatible
OPERATIOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 20.5EP-1996
CLASSIFICATION NUMBER: US 08/531,525
FILING DATE: 20.5EP-1996
PRICH APPLICATION NUMBER: US 60/004,091
FILING DATE: 21.5EP-1995
PRICH APPLICATION NUMBER: US 60/004,091
FILING DATE: 21.5EP-1995
PRICH APPLICATION NUMBER: US 60/004,091
FILING DATE: 21.5EP-1995
PRICH SETENCE (13.94) 499-8080
TELEPHONE: (3.03) 499-8080
TELEPHONE: CHARACTERICATICS:
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5310 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.48;
77.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193 PFKDDĠKPC 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 PFSPDGKPC 17
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE
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US-09-538-092-958
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Gaps ö

Length 184; 5; Indels

Score 43; DB 4; Pred. No. 25; 1; Mismatches

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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL00130, WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PELLING DATE: 2000-10-20
PRIOR PLILING DATE: 2000-10-03
PRIOR PLILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PLILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PLILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE PRESEQ for Windows Version 4.0
SEQ ID NO 7506
LENGTH: 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: March 18, 2005, 19:12:10 Job time: 42.48 secs
                                                                                                                                                                                                                                                                                                                                                                                                                           44.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 RKIENVPTGPNNKP 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7506
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                                                                                                                                                                                                                                    Patent No. 6710030
GENERAL INFORMATION:
APPLICATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: CONTORTROSTATION (CN) AND METHODS FOR ITS USE IN PREVENTING METAST
TITLE OF INVENTION: OTHER CONDITIONS
FILE REFRENCE: 1279-338CJ/09801388
CURRENT PAPLICATION NUMBER: US/09/460,295B
CURRENT FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/163,047
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Facence 13801, Application US/09489039A

Sequence 13801, Application US/09489039A

Facent No. 6610836

GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PREGMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR PILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 13801

LENGTH: 429
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Pred. No. 60;
                             2; Indels
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Best Local Similarity 60.0%; Pred. No. 59; Matches 6; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 stity 58.8%; Score 43.5; ilarity 58.8%; Pred. No. 54; Conservative 1; Mismatches
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                                                                                                                                                                                                                      ; Sequence 8, Application US/09460295B
; Patent No. 6710030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Trimeresurus gramineus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257 ERDIQTVAFSPORGOHC 273
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149 FSEDYSEIHYSPDGR 163
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                                                                                              :| |||:||
281 IPRQPDGRPC 290
                                                                 8 VPFSPDGKPC 17
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Best Local Similarity
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Best Local Similarity
Matches 7; Conserva
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US-09-489-039A-13801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Klebsi
US-09-489-039A-13801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-949-016-7506
                                                                                                                                                                           RESULT 13
US-09-460-295B-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 552
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March 18, 2005, 19:02:16; Search time 125.12 Seconds (without alignments) 44.910 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.ppp:*
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| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.ppp:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1401741 segs, 330541175 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                         - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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97
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Perfect score:
                                                                                                                                                     OM protein
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Maximum DB
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Sequence 12, Appl
Sequence 13, Appl
Sequence 1044, Ap
Sequence 3005, Ap
Sequence 20066, A
Sequence 19046, A
Sequence 19869, A
Sequence 13011, A
Sequence 4, Appli
Sequence 4, Appli
                                                                    Sequence 10, Appl
Sequence 11, Appl
                                         Description
                                                              5 US-10-839-729-10
5 US-10-839-729-11
5 US-10-839-729-12
7 US-10-808-187-1044
5 US-10-320-97-3302
5 US-10-369-493-20066
5 US-10-369-493-19869
5 US-10-369-493-19869
6 US-10-369-493-19869
7 US-10-369-493-19869
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7 US-10-369-493-19869
8 US-10-369-493-19869
8 US-10-369-493-19869
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SUMMARIES
                         Query
Match Length DB
                                                                                100.0
100.0
100.0
100.0
52.6
51.5
                                                                   97
97
97
97
97
97
88
88
                           Result
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Sequence 10, Application US/10839729
| Publication No. US2005002953A1
| GENERAL INFORMATION:
| APPLICAMT: Oran Herold
| TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
| TITLE OF INVENTION: AND METHODS OF USE
| FILE REPERENCE: BIODBANK. 013A
| CURRENT APPLICATION NUMBER: US/10/839,729
| CURRENT FILING DATE: 2004-05-04
| PRIOR APPLICATION NUMBER: 60/468703
| PRIOR FILING DATE: 2003-05-06
| NUMBER OF SEQ ID NOS: 49
| SOFTWARE: FastsEQ for Windows Version 4.0
| SEQ ID NO 10
| LENGTH: 1255 ORGANISM: SARS Coronavirus US-10-839-729-10 TYPE: PRT

Gaps ö 100.0%; Score 97; DB 16; Length 1255; 100.0%; Pred. No. 5.1e-06; tive 0; Mismatches 0; Indels 0; Best\_Local Similarity 100 Matches 17; Conservative Query Match

US-10-839-729-10

1 FERDISNVPFSPDGKPC 17

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US-10-839-729-11 ; Sequence 11, Application US/10839729 ; Enblication No. US20050002953A1 ; GENERAL INFORMATION: 451 FERDISNVPFSPDGKPC 467 ы

APPLICANT: Jens Herold

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US-10-808-187-1044
    US-10-839-729-13
                                                Query Match
                                                                                            Matches
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Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches ارکدی ماری Mismatches مارید تابید
                                                                                                                                                                                                                                                                                                                                       Length 1255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/10839729
Sequence 12, Application US/10839729
Publication No. US20050002953A1
GENERAL INFORMATION:
APPLICANT: JOHN HORMATION:
TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
TITLE OF INVENTION: ADD METHODS OF USE
FILE REFERENCE: BIODANK.013A
CURRENT APPLICATION NUMBER: US/10/839,729
CURRENT FILING DATE: 2004-05-04
PRIOR FILING DATE: 2003-05-06
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13, Application US/10839729
Publication No. US20050002953A1
GENERAL INFORMATION:
APPLICANT: Jens Harold
TITLE OF INVENTION: AND METHODS OF USE
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: BIOBANK: 013A
CURRENT APPLICATION NUMBER: US/10/839,729
CURRENT APPLICATION NUMBER: 60/468703
PRIOR PLING DATE: 2004-05-04
PRIOR FILING DATE: 2003-05-06
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 1255
TYPE: PRT

VARIE: PRT
                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES TITLE OF INVENTION: AND METHODS OF USE FILE REFERENCE: BLOBANK. 013A CURRENT APPLICATION NUMBER: US/10/839,729 CURRENT FILING DATE: 2004-05-04 PRIOR APPLICATION NUMBER: 60/468703 PRIOR FILING DATE: 2003-05-06
                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 97; DB 16;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                            NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451 FERDISNVPFSPDGKPC 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   451 FERDISNVPFSPDGKPC 467
                                                                                                                                                                                                                                                                                                                                                                                                                                1 PERDISNVPFSPDGKPC 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CRGANISM: SARS Coronavirus
US-10-839-729-12
                                                                                                                                                                                                                                                    TYPE: PRT; ORGANISM: SARS Coronavirus
US-10-839-729-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
US-10-839-729-13
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US-10-320-797-3302

US-10-320-797-3302

US-10-320-797-3302

Sequence 3302, Application US/10320797

Publication No. US20040014955A1

GENERAL INFORMATION:
APPLICATY: Exception Alexey M.
APPLICATY: Exception UDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND TITLE OF INVENTION: METHODS OF USE

TITLE OF INVENTION: METHODS OF USE

FILE REFERENCE: 10182-021-999

CURRENT APPLICATION NUMBER: US/10/320,797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: CHAN, KWOK HUNG
APPLICANT: CHAN, KWOK HUNG
APPLICANT: CHAN, KWOK HUNG
APPLICANT: CHAN, KWOK HUNG
APPLICANT: NICHOLIS, JOHN
TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
TITLE OF INVENTION: RESPIRATORY SYNDROME (SARS)
FILE REFERENCE: V9661.0078
CURRENT APPLICATION NUMBER: US/10/808,187
CURRENT APPLICATION NUMBER: 60/457,031
PRIOR FILING DATE: 2003-03-24
PRIOR FILING DATE: 2003-04-32
PRIOR PILING DATE: 2003-04-02
PRIOR APPLICATION NUMBER: 60/460,357
PRIOR APPLICATION NUMBER: 60/460,357
PRIOR PILING DATE: 2003-04-08
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   Length 1255;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 97; DB 17;
100.0%; Pred. No. 5.1e-06;
tive 0; Mismatches 0;
100.0%; Score 97; DB 16; 100.0%; Pred. No. 5.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1044, Application US/10808187 Publication No. US20050009009A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2003-04-23
PRIOR APPLICATION NUMBER: 60/471,200
PRIOR FILING DATE: 2003-05-16
NUMBER OF SEQ ID NOS: 2476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       453 FERDISNVPFSPDGKPC 469
                                                                                                                                                                                                  451 FERDISNVPFSPDGKPC 467
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                                                                                                                                              1 FERDISNVPFSPDGKPC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: PEIRIS, JOSEPH S. M. APPLICANT: YUEN, KWCK YUNG PODPLICANT: POON, YII MAN APPLICANT: GUAN, YI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin ver. 3.2 SEQ ID NO 1044
                                Local Similarity 100.
hes 17; Conservative
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Gaps

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DEPLICANT: Cao, Yongwei

APPLICANT: Alater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10 (520.5) B.

CURRENT APPLICATION NUMBER: US/10/369, 493

CURRENT APPLICATION NUMBER: US 60/360, 039

PRIOR APPLICATION NUMBER: US 60/360, 039

PRIOR APPLICATION NUMBER: US 60/360, 039

SEQ ID NO 13011

LENGTH: 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slatery S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 19869
LENGTH: 1155
                                                                                                                                                                                        Score 50; DB 15; Length 1136;
Pred. No. 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 48; DB 15; Length 1155;
Pred. No. 1.6e+02;
4; Mismatches 2; Indels (
                                                                                                                                                                                                                                         Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: No. US20030233675Altoc punctiforme
US-10-369-493-19869
                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19869, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 13011, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Aspergillus nidulans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.5%;
                                                                                                                                                                                        Query Match
Best Local Similarity 64.3%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1108 QRGVNSVSFSPDGK 1121
    PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 19046
LENCTH: 1136
TYPE: PRT
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648 EQTVNNVYFSPDGK 661
                                                                                                                                                                                                                                                                                       2 ERDISNVPFSPDGK 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 57.1.
Best Local 8; Conservative
                                                                                                                       ; ORGANISM: Anabaena PCC7120
US-10-369-493-19046
                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-369-493-19869
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Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Gao, Yongwei

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION UNMER: US/10/369,493

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20066
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                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.5%; Score 50; DB 15;
53.3%; Pred. No. 43;
iive 5; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: No. US20030233675Altoc punctiforme
                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                    NAME/KEY: MISC FEATURE
CATION: (556)...(556)
COTHER INNORMATION: Xaa = any amino acid
US-10-320-797-3302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-369-493-20066
; Sequence 20066, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION WUMBER: 60/341,261
PRIOR FILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 3361
SOFTWARE: Perentin version 3.1
SEQ ID NO 3302
LENGTH: 846
                                                                                                                                                                                           ORGANISM: Cryptococcus neoformans
                                                                                                                                                                                                                                                                                                                                                         52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:| ::| ||||||
95 FKRKVHHVSFSPDGK 109
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Best Local Similarity 60.07
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Best Local Similarity 53.34
Then 8; Conservative
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                                                                                                                                                                     TYPE: PRT
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US-10-799-62-7.
US-10-799-62-7.
Sequence 4, Application US/10798625
Publication No. US20040185146A1
GENERAL INFORMATION:
APPLICANT: PELLETIER, Marc
BARKER, William A.
HAKES, David J.
ZOPP, David A.
TITLE OF INVENTION: SIALYLOLIGOSACCHARIDES IN A DAIRY SOURCE
SIALYLOLIGOSACCHARIDES IN A DAIRY SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match

Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 9; Conservative 1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REPERRATION NUMBER: 7188-032-999
TELECOMMUNICATION INFORMATION:
TELEFAN: (212) 7909090
TELEFAX: (212) 8699741
TELEX: 66141 PENNIE
                                                                      FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7188-032-999
TELECOMUNICATION INFORMATION:
TELEPHONE: (212)790900
TELEPHONE: (212)790900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/799,625
PILING DATE: 11-MAR-2004
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/955,909
FILING DATE: 18-Sep-2001
APPLICATION NUMBER: 08/911,393
FILING DATE: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/911,393
       CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                       LENGTH: 642 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                     TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FERDISNVPFSPDGK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 FKROSSKVPFEKDGK 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-798-625-4
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Publication No. US2030233675A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gara, Yongwei
APPLICANT: Gladman, Barry
APPLICANT: Goldman, Barry
APPLICANT: Goldman, Barry
APPLICANT: Goldman, Barry
APPLICANT: Goldman, Barry
APPLICANT: Gladman, Barry
APPLICANTION
ANDRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE OF INVENTION: USA023-02-28
PRIOR FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20247
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                                                                                                                                                     Gaps
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BARKER, William A.

HAKES, David J.

ZOPF, David J.

TITLE OF INVENTION: METHODS FOR PRODUCING

SIALYLOLIGOSACCHARIDES IN A DAIRY SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                         Length 699;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 47; DB 15; Lengtn va. Pred. No. 1.26+02;
                                                                                                                                                     Indels
                                                                                                      Score 47.5; DB 15;
Pred. No. 1.1e+02;
2; Mismatches 3;
; NAME/KEY: unsure
; LOCATION: (1)..(699)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-13011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: No. US20030233675Altoc punctiforme
US-10-369-493-20247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/955,909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Amer.
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09955909
Patent No. US20020150995A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                :||| | || : ||||
137 QRDIKNYPFKVVNKDGKP 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                  2 ERDISNVPF---SPDGKP 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.5%;
                                                                                                           49.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        389 EKEVNSVAFSPDGQ 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 ERDISNVPFSPDGK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                        10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                    RESULT 11
US-10-369-493-20247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
US-09-955-909-4
                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                      Score 47; DB 16; Length 642;
Pred. No. 1.2e+02;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

47.4%; Score 46; DB 14; Length 120;
Best Local Similarity 64.3%; Pred. No. 29;
Matches 9; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-10-083-357-1281
; Sequence 1281, Application US/10083357
; Publication No. US20030054370A1
; GENERAL INFORMATION:
; APPLICANT: Qiandong Zeng et al.
; TITLE REPRENCE: 032796-090
; CURRENT APPLICATION NUMBER: US/10/083,357
; CURRENT FILING DATE: 2002-02-7
; NUMBER OF SEQ ID NOS: 1346
; SEQ ID NO 1281
; LENGTH: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCHOOLS AND ADDICATION US/10156761
FUDIcation No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: INFORMATION:
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REBERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILING DATE: 2001-05-30
FRIOR FILING DATE: 2001-05-30
FRIOR FILING DATE: 2001-05-30
FRIOR FILING DATE: 2001-05-30
FRIOR FILING DATE: 2001-05-30
FRIOR SEQ ID NOS: 15109
| INFORMATION FOR SEQ ID NO: 4:
| SEQUENCE CHARACTERISTICS:
| ILENGTH: 642 amino acids
| TYPE: amino acids
| TYPE: amino acid
| STRANDEDNESS: single
| TOPOLOGY: linear
| MOLECULE TYPE: protein
| SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-083-357-1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 60.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                        1 FERDISNVPFSPDGK 15
                                                                                                                                                                                                                                                                                                                                                                                              12 FKRQSSKVPFEKDGK 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ERDISNVPFSPDGK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :| || | |||||:
8 QRKISAVKFSPDGR 21
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US-10-156-761-9368
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47.4%; Score 46; DB 14; Length 396;

Query Match

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Best Local Similarity 50.0%; Pred. No. 16+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps
Qy 4 DISNVPFSPDGKPC 17
| | ... | | | ... | | ... | | ... | | ... | | ... | | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | .
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
             Copyright
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- protein search, using sw model OM protein March 18, 2005, 18:59:20 ; Search time 33.32 Seconds (without alignments) 49.090 Million cell updates/sec Run on:

US-10-773-274A-2 97 score: Title: Perfect sc Sequence:

1 FERDISNVPFSPDGKPC 17

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
	50	51.5	1683	. ~	AF2071	WD-40 repeat prote
7	48	49.5	736	7	D96830	u
٣	48	49.5	831	64	E96830	hypothetical prote
4	47.5	49.0	570	7	C90485	beta-glucuronidase
S	47	48.5	134	7	E81133	hypothetical prote
9	47	48.5	919	7	AH2195	hypothetical prote
7	46	47.4	132	7	MFIV2J	•-
8	46	47.4	571	~	S24789	jararhagin C precu
6	46	47.4	831	7	S74252	heat shock protein
10	46	47.4	1329	7	AE1901	WD-repeat containi
11	45.5	46.9	377	N	AF2273	hypothetical prote
12	45	46.4	207	~	S40747	
13	45	46.4	275	7	A36264	DNA-directed RNA p
14	45	46.4	275	~	JC6181	ase I
15	45	46.4	288	Н	SNBYC1	proteasome endopep
	45	46.4	337	N	D69284	conserved hypothet
17	45	46.4	934	~	AG1889	WD-40 repeat prote
18	45	46.4	196	N	E86245	
19	44	45.4	395	N	T23317	
20	44	45.4	480	-1	A30065	trigramin precurso
21	44	45.4	586	N	T38992	WD-40 repeat regul
22	44	45.4	594	~	850802	hypothetical prote
23	44	45.4	613	~	S50721	dnaK-type molecula
24	44	45.4	613	~	S20149	dnaK-type molecula
25	43.5	44.8	470	7	C97032	Fe-S oxidoreductas
26	43	44.3	28	7	849347	ccoQ protein - Rho
27	43	44.3	103	7	G84741	hypothetical prote
28	43	44.3	355	~	27	
29	43	44.3	407	~	866260	

atrolysin C (EC 3. atrolysin C (EC 3.		serine-type D-Ala- fibrinolytic metal	metalloproteinase-	catrocollastatin p	hypothetical prote	WD-40 repeat prote	WD-40 repeat prote	probable GTPase-ac	exopolyphosphatase	hypothetical prote	guanylate kinase T	WD-40 repeat prote	glyceraldehyde-3-p
HYRSAC S41609	841608	JN0801 JC4880	JC8020	S55270	B96625	AE1810	AC1842	T14106	C97356	E83566	F81718	AG1837	DEASG3
н 0	ο,	п 0	7	~	~	N	~	N	N	~	~	~	-
414	414	452 478	484	609	867	1227	1747	1822	661	111	205	304	336
44.3	44.3	44. 44.3	44.3	44.3	44.3	44.3	44.3	44.3	43.8	43.3	43.3	43.3	43.3
4 4 3 6	43	4 4 U E	43	43	43	43	43	43	42.5	42	42	42	42
30	32	33 4	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

_	
	71
S	2071

WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004

C,Accession: AF2071
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchı Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AF2071

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-1683 <KUR>

A,Cross-references: UNIPROT: 08YV57; GB:BA000019; PIDN:BAB73823.1; PID:gl7131215; GSPDB:GA,Experimental source: strain PCC 7120

C,Genetics: A,Gene: all2124

Gaps ö Length 1683; 2; Indels 51.5%; Score 50; DB 2; 64.3%; Pred. No. 15; tive 3; Mismatches Conservative Query Match Best Local Similarity Matches 9; Conserv

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|: ::|| |||||| 1155 EQTVNNVYFSPDGK 1168 2 ERDISNVPFSPDGK 15 8

셤

probable heat-shock protein, 41956-44878 [imported] - Arabidopsis thaliana C'Species: Arabidopsis thaliana (mouse-ear cress)
R'Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Hujar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.A.; Liu, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Liuros, J.S.; Maiti, R.; Marziali, Rizo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A,Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A,Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A,Accession: D96830

A;Status: preliminary

A;Cross-references: UNIPROT: Q9CA95; GB: AE005173; NID: g6453874; PIDN: AAF09058.1; GSPDB:GN

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Gaps

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R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Science 207, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Vei A;Authors: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Mosidues: 1-134 «TET»
A;Rosidues: 1-134 «TET»
A;Cross-references: UNIPROT: 09JZM1; GB:AE002450; GB:AE002098; NID:97226229; PIDN:AAF4139
A;Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. Aya Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross_references: UNIPROT:Q8YSG6; GB:BA000019; PIDN:BAB74818.1; PID:g17132214; GSPDB:GA;Experimental source: strain PCC 7120
C;Genetics:
                                                                                                                                                                                                                                              hypothetical protein NMB0990 [imported] - Neisseria meningitidis (strain MC58 serogroup C, Species: Neisseria meningitidis C, Date: 31-Mar-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein alr3119 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AH2195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: NWB0990
C;Superfamily: Neisseria meningitidis hypothetical protein NMAll91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length. 134;
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Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.5%; Score 47; DB 2; 50.0%; Pred. No. 2.8; tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .,
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Pred. No. 17;
2; Mismatches
Mismatches
4;
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ilarity 72.7%;
Conservative
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216 FEKDVNNVIPWSPD 229
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99 ERDLCKIPFPPDSR 112
                                                       1 FERDISNV-PFSPD 13
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520 VANVAFSPDGK 530
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Best Local Similarity
8; Conserve
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nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                      C; Accession: E81133
  6
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Matches
  Matches
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C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-0201 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Date: 24-0201 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Date: 25-0201 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Date: 25-0201 #sequence_revision 25-0301 #text_change 09-Jul-2004
C;Date: 25-0201 #sequence_revision 25-0301 #text_change 09-Jul-2004
A;Cesesion: C;Date: A; Ragan, M.A.; Sensen, C.W.; Wan der Oost, J.
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: C;D4485
A;Residues: 1-570 *KUR>
A;Molecule type: DNA
A;Residues: 1-570 *KUR>
A;Ceses-references: UNIPROT:Q97UII; GB:AE006641; NID:g13816434; PIDN:AAK43138.1; GSPDB:GCGGNETERICS:
A;Genetics:
A;Genetics:
A;Gene: gusB
C;Superfamily: beta-glucuronidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cjaccesion: E96830
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Rer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: E96830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F18B13.1 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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49.5%; Score 48; DB 2; Length 831;
Best Local Similarity 52.6%; Pred. No. 15;
Matches 10; Conservative 3; Mismatches 2; Indels
                                                                                                                                           DB 2; Length 736
                                                                                                                                                                                                2; Indels
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Pred. No. 12;
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Pred. No.
                          A,Gene: F19K16.12
A,Map position: 1
C,Superfamily: heat shock protein 91
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64.3%;
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al Similarity 52.6%;
10; Conservative
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A;Molecule type: DNA
A;Residues: 1-831 <STO>
A;Cross-references: UNIPR
C;Genetics:
                                                                                                                                        Query Match
Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
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A; Map position: 1
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Gaps

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Gaps
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C;Species: influenza C virus
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F;295,299,305/Binding site: zinc (His) #status predicted F;296/Active site: Glu #status predicted
                                                                                       47.4%; Score 46; 46.7%; Pred. No.
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81 QRDIKSFPFSVTEGPDGYP 99
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C; Keywords: heat shock
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649 KEVNDVAFSPDGK 661
                                                                  Query Match
Best Local Similarity 46.77
Best Local 7; Conservative
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Best Local Similarity
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Best Local Similarity
7; Conserve
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A; Residues: 1-831 <STO>
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NyAlternate names: single chain botrocetin
NyContains: disintegrin-like 28K protein; hemorrhagic proteinase (EC 3.4.24.-)
C;Species: Bothrops jararaca (jararaca)
C;Date: 20-Feb-1995 #Bequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C;Accession: S24789; JC2245; Ā44463; A37958; JC2373
R;Paine, M.J.I.
R;Paine, M.J.I.
R;Paine, M.J.I.
R;Paine, M.J.I.
R;Paine, M.J.I.
A;Accession: S24789
A;Accession: S24789
A;Accession: S24789
A;Reference number: S24789
A;Reference: UNIPROT: P30431; EMBL:X68251; NID:g62467; PID:g62468
R;Usami, Y.; Fujimura, Y.; Miura, S.; Shima, H.; Yoshida, E.; Yoshioka, A.; Hirano, K.;
Biochem. Biophys. Res. Commun. 201, 331-339, 1994
A;Itle: A 28 kDa-protein with disintegrin-like structure (jararhagin-C) purified from E
A;Reference number: JC2245; MUID:94256999; PMID:8198592
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R; Fujimura, Y.; Titani, K.; Usami, Y.; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui, H.; Sug Biochemistry 30, 1957-1954, 1991

A; Title: Isolation and chemical characterization of two structurally and functionally di A; Reference number: A17958; MUID:91129280; PMID:1993206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Experimental source: venom
R;Paine, M.J.; Desmond, H.P.; Theakston, R.D.; Crampton, J.M.
J. Biol. Chem. 267, 22869-22876, 1992
A;Title: Purification, cloning, and molecular characterization of a high molecular weigh
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 21-Nov-1997
C;Accession: B2878
R;Yamashita, M.; Krystal, M.; Palese, P.
J. Virol. 62, 3348-3355, 1988
A;Title: Evidence that the matrix protein of influenza C virus is coded for by a spliced A;Reference number: A93036; MUID:88300888; PMID:3404579
A;Accession: B28878
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A;Residues: 1-23,'Q',25-92,'G',94-131,'G',133-169,'Q',171-571 <PA2>
A;Cross-references: GB:X68251
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A;Mesidues: 360-372, E',374-378, 'X',380-384 <FUJ>
A;Mesidues: 361-Val was also found
C;Comment: Inhibits collagen- and ADP-induced platelet aggregation.
C;Superfamily: mouse meltrin alpha; disintegrin homology
C;Superfamily: mouse metalloproteinase; venom; zinc
F;360-571/Product: jararhagin C #status experimental <MAT>
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A Residues: 1-132 < YAM>
A Cross-references: GB M22038; NID:9325303
A;Note: this ORF is not annotated in GenBank entry FLCCJUM C;Genetics:
A,Map position: segment 6
C;Superfamily: influenza C virus matrix protein M2
C;Keywords: matrix protein
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Pred. No. 4;
1; Mismatches
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116 ETDISPIPFSNDG 128
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Best Local Similarity
Matches 9, Conserva
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                                                                                                                                                                                                         A; Molecule type: mRNA
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Ristorozhenko, S.; de Pauw, P.; Kushnir, S.; van Montagu, M.; Inze, D.
FBBS Lett. 390, 113-118, 1996
A'fille: Identification of an Arabidopsis thaliana cDNA encoding a HSP70-related protein
A'Reference number: S74252; WUID:96314561; PMID:8706819
A'Accession: S74252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT: Q96269; EMBL: Z70314; NID:g1495250; PIDN: CAA94389.1; PID:g149
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K;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, T.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
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A;Residues: 1-1329 «KUR»
A;Cross-references: UNIPROT:QSYYT7; GB:BA000019; PIDN:BAB72716.1; PID:g17130104; GSPDB:C
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all0759
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C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 28-Oct-1996 #sequence_revision 14-Nov-1997 #text_change 09-Jul-2004
                                                               Gape
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Length 571;
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53;
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   5
Score 46; DB 2
Pred. No. 20;
4; Mismatches
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Pred. No. 53;
5; Mismatches
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2 ERDISNVPFSPDGKP 16
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Best Local Similarity 46.7
Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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hypothetical protein all3741 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AF2273
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
                                                                                                                                                                                                                                                                                                                    DNA Res. 8, 205-213, 2001

A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807; MUD:21595285; PMID:11759840

A; Reference number: AB2273

A; Status: preliminary
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-377 <KUR>
A; Cross-references: UNIPROT:Q8YQS8; GB:BA000019; PIDN:BAB75440.1; PID:g17132875; GSPDB:GCGenetics:
C; Genetics:
A; Experimental source: strain PCC 7120
C; Genetics:
A; Genetics:
C; Superfamily: Campylobacter jejuni hypothetical protein Cj1270c
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C;Species: Genochabditis elegans
C;Species: Genochabditis elegans
C;Species: G6-Fb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C;Accession: 840747
R;Berks, M.; Smith, A.
submitted to the EMBL Data Library, February 1992
A;Reference number: 840747
A;Accession: 540747
A;Accession: 540747
A;Accession: 540747
A;Residues: 1-207 AER>
A;Residues: 1-207 AER>
A;Construction: 1-207 AER>
A;Construction: 1-207 ABR>
C;Genetics: Canericaning protein; translation elongation factor Tu homology
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Keywords: GTP binding; nucleotide binding; P-loop
F;20-27/Region: GTP-binding NCXD motif
F;126-129/Region: GTP-binding NCXD motif
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Cispecies: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 09-Jul-2004
Cispecies: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 09-Jul-2004
Cispecies: Air and the same of the homan RNA polymerase II 33-kDa subunit hRPB 3A; Reference number: A36264; MUID:90256750; PMID:2187864
A; Reference number: A36264
A; Reference mumber: A36264
A; Re
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46.4%; Score 45; DB 2
Best Local Similarity 77.8%; Pred. No. 9.5;
Matches 7; Conservative 0; Mismatches
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Best Local Similarity 66.7
Matches 10; Conservative
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A;Cross-references: UNIPROT:P19387; GB:J05448; NID:g337496; PIDN:AAA36586.1; PID:g337497 C;Superfamily: DNA-directed RNA polymerase II, RPB3 subunit; ferredoxin 2[4Fe-4S] homolo C;Keywords: nucleotidyltransferase; transcription
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A;Residues: 1-275 - KOR>
A;Cress-references: UNIPROT: P97760; DDBJ:D83999; NID:g1850788; PIDN:BAA12205.1; PTD:g185.
C;Superfamily: DNA-directed RNA polymerase II, RPB3 subunit; ferredoxin 2[4Fe-4S] homolo
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A;Residues 1-288 «FUJ»
A;Cross-references: UNIPROT:P21242; EMBL:M55436; NID:g173203; PIDN:AAA35227.1; PID:g1732
A;Accession: A38769
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A;Residues: 1-288 <DEL>
A;Cross-references: EMBL:Z75270; NID:g1420785; PIDN:CAA99691.1; PID:g1420786; GSPDB:GN00
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AjCross-references: SGD:S0005889; MIPS:YOR362c
AjArcoss-references: SGD:S0005889; MIPS:YOR362c
CjSuperfamily: multicatalytic endopeptidase complex chain C9
CjSuperfamily: multicatalytic endopeptidase; proteasome; protein degradation; proteinase
F;2-288/Product: multicatalytic endopeptidase complex chain YC1 #status predicted <MAT>F;2/Modified site: blocked amino end (Thr) (in mature form) #status experimental
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A,Residues: 105-134;179-194;199-208 <FUJZ>
R;Delius, H.; Hebling, U.; Hofmann, B.
submitted to the Protein Sequence Database, July 1996
A,Reference number: S67261
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46.7%; Pred. No. 13;
tive 3; Mismatches
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Query Match 46.4%; Score 45; DB 1; Length 288; Best Local Similarity 66.7%; Pred. No. 14; Matches 8; Conservative 2; Mismatches 2; Indels
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(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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                                                   - protein search, using sw model
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seq length: 200000000
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	Q6va78 sars corona	Q6va89 BarB corona	Qévaa0 sars corona	Q6wgp3 sars corona	P83692 thielavia h	Q8tmx4 methanosarc	Q6fy54 candida gla			Q6udw6 plasmodium			Q987c0 arabidopsis	Q8p8t6 xanthomonas
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	97	97	97	97	55	52	20	20	49	49	48	48	48	48
	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

```
STRAIN=Isolate Tor2;

MEDLINE=22660725; PubMed=12730501; DOI=10.1126/science.1085953;

A Marta M.A., Jones S.J.M., Ratell C.R., Holl R.A., Brooks-Wilson A.,

Butterfield Y.S.N., Khattra J., Asano J.K., Barber S.A., Chan S.Y.,

Cloutier A., Coughlin S.M., Freeman D., Girn N., Griffith O.L.,

Leach S.R., Mayo M., McDonald H., Montgomery S.B., Pandoh P.K.,

A Petrescu A.S., Robertson A.G., Schein J.E., Siddiqui A., Smailus D.E.,

Stott J.M., Yang G.S., Plummer F., Andonov A., Artsob H., Bastien N.,

Bernard K., Booth T.F., Bowness D., Czub M., Drebot M., Fernando L.,

Flick R., Garbutt M., Gray M., Grolla A., Jones S., Feldmann H.,

A Flick R., Garbutt M., Ward D., Watson B., Brunham R.C., Krajden M.,

Petric M., Skowronski D.W., Upton C., Roper R.L.;

"The genome sequence of the SARS-associated coronavirus.";
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SETAAIN=ISOJATE Urbani;
MEDLINE=22660724; PubMed=12730500; DOI=10.1126/science.1085952;
Rota P.A., Oberste M.S., Monroe S.S., Nix W.A., Campagnoll R.,
Icenogle J.P., Penaranda S., Bankamp B., Maher K., Chen M.-H.,
Icenogle J.P., Peret T.C.T., Frace M., DeRisi J.L., Chen M.-H.,
Fudman D.D., Peret T.C.T., Burns C., Kaiazek T.G., Rollin P.E.,
Sanchez A., Liffick S., Holloway B., Limor J., McCaustland K.,
Olsen-Rasmussen M., Pouchier R., Guenther S., Osterhaus A.D.M.E.,
Drosten C., Pallansch M.A., Anderson L.J., Bellini W.J.;
"Characterization of a novel coronavirus associated with severe acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=ISOLATE CUHK-Sul0, and Isolate CUHK-W1;
MEDLINE=22737955; PubMed=12853594; DOI=10.1056/NEJM200307103490216;
Tsul S.K.W., Chim S.S.C., Lo Y.M.D.;
"Coronavirus genomic-sequence variations and the epidemiology of the severe acute respiratory syndrome.";
N. Engl. J. Med. 349:187-188(2003).
                                                                                                                                                                                   Human coronavirus (strain SARS) (HCOV-SARS) (SARS-COV).
Viruses; ssRNA positive-etrand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                           E2 glycoprotein precursor (Spike glycoprotein) (Peplomer protein) Name=S;
                                                            P59594; Q77696; Q77A19; Q77FA2; Q77FB1; Q80BV6; U10-0CT-2003 (Rel. 42, Created) 10-0CT-2003 (Rel. 42, Last sequence update) 25-0CT-2004 (Rel. 45, Last annotation update)
                                            PRT; 1255 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  respiratory syndrome.";
Science 300:1394-1399(2003).
                                            STANDARD;
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SEQUENCE FROM N.A
                                          CVHSA
RESULT 1
VGL2 CVHSA
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ERRATUM.
PubMed=12781581;
Ruan X., Wei C.L., Ling A.E., Vega V.B., Thoreau H., Se Thoe S.Y.,
Chia J.-M., Ng P., Chiu K.P., Lim L., Zhang T., Chan K.P., Oon L.E.L.,
Ng M.L., Leo S.Y., Ng L.F.P., Ren E.C., Stanton L.W., Long P.M.,
STRAIN=Isolate HKU-39849;
MEDLINE=22758472; PubMed=12876307;
Zeng F.Y., Chan C.W., Chan M.N., Chan J.D., Chow K.Y.C., Hon C.C.C.,
Hui R.K.H., Li J., Li J., Li V.Y.Y., Wang C.Y., Wang P.Y., Guan Y., Zheng B.,
Poon L.L.M., Chan K.H., Yuen K.Y., Peiris J.S.M., Leung F.C.;
"The complete genome sequence of severe acute respiratory syndrome coronavirus strain HKU-39849 (HK-39).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=ISOlate Sin2500, Isolate Sin2677, Isolate Sin2679, Isolate Sin2748, and Isolate sin2774; MEDLINE=22667074; PubMed=12781537; DOI=10.1016/S0140-6736(03)13414-9; Ruan Y., Wei C.L., Ling A.E., Yoga v.B., Thoreau H., Se Thoe S.Y., Chia J.-M., Ng P., Chiu K.P., Lim L., Zhang T., Chan K.P., Oon L.B.L., Ng M.L., Leo S.Y., Ng L.F.P., Ren B.C., Stanton L.W., Long P.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-ISOJACE BJ01, Isolate BJ02, Isolate BJ03, Isolate BJ04, and Isolate GD01;
GD01;
GD01;
GD01;
GD01;
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GD03;
GD0
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Yeh S.-H., Kao C.-L., Tsai C.-Y., Liu C.-J., Chen D.-S., Chen P.-J.;
"The complete genome of SARS coronavirus clone TW1.";
"The Complete GNAY-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Comparative full-length genome sequence analysis of 14 SARS coronavirus isolates and common mutations associated with putative origins of infection." ("). Lancet 361:1779-1785 (2013).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-ISOlate FRA;
STRAIN-ISOlate FRA;
SICKMann M., Becker S., Klenk H.-D., Doerr H.W., Stadler K.,
Censini S., Guidotti S., Masignani V., Scarselli M., Mora M.,
Donati C., Han J., Song H.C., Abrignani S., Covacci A., Rappuoli
"SARS virus is a close relative of type II coronaviruses.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=Isolate Frankfurt 1;
Thiel V., Hertzig T., Putics A., Ivanov K.A., Schelle B., Bayer
Scheiner B., Weinand H., Weissbrich B., Ziebuhr J.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                            SEQUENCE FROM N.A.
STRANT=Stolate GZ50, and Isolate HKU-36871;
MEDLINE=18041et GZ50, bubwed=12958366; DOI=10.1126/science.1087139;
Guan Y., Zheng B.J., He Y.O., Liu X.L., Zhuang Z.K., Cheung C.L.
Luo S.W., Li P.H., Zhang L.J., Guan Y.J., Butt K.M., Wong K.L.,
Chan K.W., Lim W., Shortridge K.F., Yuen K.Y., Peiris J.S.M.,
Poon L.L.M.
                                                                                                                                                                                                                                                                                                                                                   "Isolation and characterization of viruses related to the SARS
                                                                                                                                                                                                                                                                                                                                                                       coronavirus from animals in southern China."; Science 302:276-278(2003).
                                                                                                                                                      Exp. Biol. Med. 228:866-873(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lancet 361:1832-1832(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Isolate Taiwan TC3;
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Yuan Z., Zhang X., Hu Y., Lan S., Wang H., Zhou Z., Wen Y.;
Yuan Z., Zhang X., Hu Y., Lan S., Wang H., Zhou Z., Wen Y.;
"Analysis of SARS coronavirus genome in Shanghai isolates.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Structural protein that makes spikes at the surface of the virus. Determines enteropathogenicity and virulence of the virus (Potential).
-:- SUBCELIULAR LOCATION: Type I membrane protein.
-!- DOMAIN: The spike SI domain displays the specificity for the host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEGUENCE FROM N.A.
STRAIN=Isolate TWC2, and Isolate TWC3;
Yang J.-Y., Lin J.-H., Chiu S.-C., Wang S.-F., Lee H.-C., Lin Y.-C.,
Yang J.-Y., Chen H.-Y., Chen P.-J., Su I.-J.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
                                                                            Yang J.-Y., Lin J.-H., Chiu S.-C., Wang S.-F., Lee S.C., Lin Y.-C., Hsu C.-K., Chen H.-Y., Chang J.G., Chen P.-J., Su I.-J., "Genomic sequence of SARS isolate from the first fatal case in
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=Isolate ZJ01;
Cong L.-M., Ding G.-Q., Lu Y.-Y., Weng J.-Q., Yan J.-Y., Hu N.-P., Wo J.-E., Chen S.-Y., Zhang Y.-J., Mei L.-L., Wang Z.-G., Yao J., Zhu H.-P., Lu Q.-Y., Li M.-H., Gong L.-M., Shi W., Li L.-J., Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- DOMAIN: The leucine zipper-like heptad repeats may mediate the fusion of viral and cellular membranes.
-1- SIMILARITY: Contains 1 spike S1 domain.
-1- SIMILARITY: Contains 1 spike S2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Isolate Taiwan TC1, Isolate Taiwan TC2, and Isolate T. Chang J.-G.C., Lin T.-H., Chen C.-M., Lin C.-S., Chan W.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Isolate Shanghai LY; Yuan Z., Wang H., Zhou Z., Wen Y.; Yuan Z., Zhang X., Hu Y., Lan S., Wang H., Zhou Z., Wen Y.; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Isolate TWH, Isolate TWJ, Isolate TWK, Isolate TWS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Balotta C., Corvasce S., Violin M., Galli M., Moroni M., Vigevani G.M., Ruan Y.J., Salemi M.; Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shu H.Y., Wu K.M., Tsai S.F.; submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Isolate HSR 1;
Canducci F., Clementi M., Poli G., Vicenzi E.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                        to the EMBL/GenBank/DDBJ databases
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                                                 STRAIN=Isolate TWC;
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SEQUENCE F
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EMBL, AYS9412; AAT52330.1; -...
GO; GO:0015621; C:integral to membrane; IEA.
GO; GO:0019031; C:virtal anvelope; IEA.
GO; GO:006894; P:membrane fusion; IEA.
GO; GO:00686813; P:virtion attachment, binding of host cell sur. . .; IEA.
InterPro; IPR02552; Corona_S2.
Pfam; PF01601; Corona_S2; 1.
SEQUENCE 1255 AA; 139170 MM; 90AFAB62485B525D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jin W.W., Feng J.D., Du Z.L., Hu L.X., Liu Y.X., Liu Y.F., Zhang X.M., Gao H., Ning Y., Zhang J.S., Li N., Yin W.D.; Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AY48578, AAR23288.1, -
GO; GO:019031; C:integral to membrane; IEA.
GO; GO:019031; C:viral envelope; IEA.
GO; GO:006944; P:membrane fusion; IEA.
GO; GO:0046813; P:virion attachment, binding of host cell sur. .; IEA.
InterPro; IPR002525; Corona, S2.
Pfam; PF01601; Corona, S2; 1.

ERQUENCE 1255 AA; I39124 MW; 1C49ACA2CFD38FC0 CRC64;
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Coronaviridae; Coronavirus.
NCBI_TaxID=255729;
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ORNames-SARSCOVGp04;
SARS coronavirus LLJ-2004.
Viruses; BRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
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        Length 1255;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
        100.0%; Score 97; DB 2; I 100.0%; Pred. No. 1.7e-06;
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                                                                                               Mismatches
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        Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
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Best Local Similarity 100.
Matches 17; Conservative
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Song H., Ling N., Li Y., Zhu J., Wang E.;
Song H., Ling N., Li Y., Zhu J., Wang E.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY648300; AAT74874.1; -.
GO; GO:0019031; C:integral to membrane; IEA.
GO; GO:0019031; C:integral to membrane; IEA.
GO; GO:0046944; P:membrane fuelon; IEA.
GO; GO:0046813; P:virion attachment, binding of host cell sur. .; IEA.
InterPro; IPRO02552; Corona S.; I.
SEQUENCE 1255 AA; J39052 MW; 4587B501B7309C4D CRC64;
                                                                                                                                                                             Gaps
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Coronaviridae; Coronavirus.
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Coronaviridae; Coronavirus.
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
BMBL, ANSS4624; AAT76147.1;
COS GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005944; P:membrane fusion; IEA.
GO; GO:0046813; P:virion attachment, binding of host cell sur.
InterPro; IPR00252; Corona S2.
Ffam; PF01601; Corona S2.
SEQUENCE 1255 AA; 139153 MW; 508759C700289A0E CRC64;
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Chen W., Yan M., Liu M.,
"Isolation and Identification of Viruses Related to the SARS
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                                                                                               Length 1255;
                                                                                      Query Match 100.0%; Score 97; DB 1; Length 12
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 17; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.7e-06;
iive 0; Mismatches 0; Indels
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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EMBL; AY278741; AAP13441.1; -.
                                                                                                                                                                                                                                                                                                                                          451 FERDISNVPFSPDGKPC 467
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Best Local Similarity 100.
Matches 17; Conservative
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SARS coronavirus TJF.
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Q692E4;
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RESULT 3

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Pfam; PF01601; Corona S2; 1.
SEQUENCE 1255 AA; 139124 MW; 1C49ACA2CFD38FC0 CRC64;
                           1 FERDISNVPFSPDGKPC 17
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GO:0019031; C:viral envelope; IEA.
GO:0006944; P:membrane fusion; IEA.
GO:0046813; P:virion attachment, binding of host cell sur. . .; IEA.
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Jin W.W., Peng J.D., Du Z.L., Hu L.X., Liu Y.X., Liu Y.F., Zhang X.M.,
Jon W.W., Peng J.D., Du Z.L., Hu L.X., Liu Y.X., Liu Y.F., Zhang X.M.,
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, 74485277; ARA2350.1;
EMBL, 74485277; ARA2350.1;
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0016021; C:integral envelope; IEA.
GO, GO:0016044; P:membrane fusion; IEA.
                                                 Gaps
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Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
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100.0%; Score 97; DB 2; Length 1255;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 17; Conservative 0; Mismatches 0; Indels
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  Length 1255;
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SEQUENCE 1255 AA; 139048 MW; 80E6F04D325D3E00 CRC64;
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Pfam; PF01601; Corona S2; 1.
SEQUENCE 1255 AA; I39173 MW; DD62DB871695C3A5 CRC64;
                                             0; Indels
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Last annotation update)
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  100.0%; Score 97; DB 2; I
100.0%; Pred. No. 1.7e-06;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                   451 FERDISNVPFSPDGKPC 467
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                                                                                          1 FERDISNVPFSPDGKPC 17
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SARS coronavirus Sinol-11.
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Best Local Similarity 100.
Matches 17; Conservative
Query Match
Best Local Similarity 100.
Matches 17; Conservative
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Q6JH46
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SEQUENCE FROM N.A.

Pubmed=14983045; DOI=10.1073/pnas.0307904100;

National Taiwan University SARS Research Team;

Yeb S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,

Yeb S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,

Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;

"Characterization of severe acute respiratory syndrome coronavirus

genomes in Taiwan: molecular epidemiology and genome evolution.";

Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).

EMBL; ARR876001; -.

GO; GO:0016021; C:integral to membrane, IEA.

GO; GO:0016021; C:integral to membrane, IEA.

GO; GO:0016031; C:viral envelope; IEA.

GO; GO:0016944; P:membrane fusion; IEA.

GO; GO:0046813; P:virion attachment, binding of host cell sur. . .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhraiman. The C., Ding R., Wang W., Li W., Wang J., Tao W., Yu X., Guo H., Chen J., Wei W., Li J., Zhang Y., Wang X., Sun Y., Jiao J., Sunag Y., Zhou C., Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AN508724; AAR91586.1; -.

EMBL; AN508724; AAR91586.1; -.

EMBL; AN508724; PAR91586.1; -.

EMBL; EMBL; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AN508724; PAR91586.1; -.

GO; GO:00109031; C:viral envelope; IEA.

GO; GO:0010813; P:virion attachment, binding of host cell sur. . .; IEA.

HIGHPRO, IPRO2552; Corona S2.

Pfam; PF01601; Corona S2: 1.

ERQUENCE 1255 AA; I39087 MW; 7C49A690C54F25C1 CRC64;
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Coronaviridae; Coronavirus.
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                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative spike glycoprotein.
SARS coronavirus TW9.
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451 FERDÍSNVPFSPDGKPC 467
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Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=260743;
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Gaps

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Indels

Length 1255;

Q6RCX6; Q6RCX6

RESULT 10

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PubMed=14983045; DOI=10.1073/pnas.0307904100;
National Taiwan University SARS Research Team;
Value S.-H., Wang H.-Y., Teai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
Su I.-J., Teai S.-F., Chen D.-S., Chen P.-J.;
"Characterization of severe acute respiratory syndrome coronavirus
genomes in Taiwan: molecular epidemiology and genome evolution.";
Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).

EMBL; AY502293 AAR875671; -.
GO; GO:0015031; C:integral to membrane; IEA.
GO; GO:0015031; C:viral envelope; IEA.
GO; GO:000544; P:membrane fusion; IEA.
GO; GO:0046813; P:virion attachment, binding of host cell sur. . .; IEA.
                                      GO; GO:0046813; P:virion attachment, binding of host cell sur. . .; IEA.
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Coronaviridae; Coronavirus.
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                                                                         Interpro, IPR002552; Corona S2.
Pfam; PF01601; Corona S2; 1.
SEQUENCE 1255 AA; 139124 MW; 1C49ACA2CFD38FC0 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative spike glycoprotein.
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05-JUL-2004 (TrEMBLrel. 27, LaBt sequence update)
05-JUL-2004 (TrEMBLrel. 27, LaBt annotation update)
Putative spike glycoprotein.
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100.0%; Pred. No. 1.7e-06;
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Best Local Similarity 100.0
Matches 17; Conservative
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Best Local 17; Conservative
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National Taiwan University SARS Research Team;
Validianal Taiwan University SARS Research Team;
Veh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
"Characterization of severe acute respiratory syndrome coronavirus
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Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).

EMBL; AY502931; AAR87589.1; -
GO; GO:001031; C:integral to membrane; IEA.
GO; GO:001031; C:virial envelope; IEA.
GO; GO:000644; P:membrane fusion; IEA.
GO; GO:0046813; P:virion attachment, binding of host cell sur. . .; IEA.
DIGERFOR DEFORMATION COLORARY.
                                                                                                                        Gaps
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Nutional Taiwan University SARS Research Team;
Yeb S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
"Characterization of severe acute respiratory syndrome coronavirus
genomes in Taiwan: molecular epidemiology and genome evolution.";
EMBL, AY502930; AAR87578.1; -. 101:2542-2547(2004).
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0016044; P:membrane fusion; IEA.
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Coronaviridae; Coronavirus.
NCBI_TaxID=258971;
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Coronaviridae; Coronavirus.
NCBL_TaxID=258970;
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                                  Length 1255;
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(TrEMBLrel. 27, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                         100.0%; Score 97; DB 2; L
100.0%; Pred. No. 1.7e-06;
iive 0; Mismatches 0;
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SARS coronavirus TW8.
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SARS coronavirus TW7.
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Matches 17; Conservative
                                                                                                                        Conservative
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Query Match
Best Local Similarity
Watches 17; Conserve
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Gaps

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RESULT 11
OGECY7
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EMBL: AYSOS27; AAR87545.1; --
GG; GO:0016021; C:integral to mebrane; IEA.
GG; GO:0019031; C:integral to mebrane; IEA.
GG; GO:0019031; C:viral envelope; IEA.
GG; GO:0019031; C:viral envelope; IEA.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative spike glycoprotein.
SARS coronavirus TW3.
Viruses; SRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronavirdae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
NCBI_TaxID=258967;
Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).

EMBL, AYS02928; AAR87556.1; --
GO; GO:001601; C:integral to membrane; IEA.
GO; GO:001691; C:viral envelope; IEA.
GO; GO:006944; P:membrane fusion; IEA.
GO; GO:0046813; P:viral artachment, binding of host cell sur.
InterPro; IPR002552; Corona S2.
Ffam; PF01601; Corona S2; 1.
SEQUENCE 1255 AA; I39124 MW; 1C49ACA2CFD38FC0 CRC64;
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Local Similarity 100.0%; Pred. No. 1.7e-06;
Ne 17; Conservative 0; Mismatches 0; Indels
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative spike glycoprotein.
SARS coronavirus TW4.
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SEQUENCE FROM N.A.
PubMed=14983045; DOI=10.1073/pnas.0307904100;
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Best Local Similarity 100...
Best Local 17; Conservative
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National Taiwan University SARS Research Team,
Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
Su I.-J., Tasi S.-F., Chen D.-S., Chen P.-J.;
InterPro, Tasi S.-F., Chen D.-S., Chen P.-J.;
"Characterization of severe acute respiratory syndrome coronavirus
genomes in Taiwan: molecular epidemiology and genome evolution.";
Proc. Natl. Acad. Sci. US.A. 101:2542-2547(2004).

EMBL; AX502926; AAR87534.1; -
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0006944; P:membrane fusion; IEA.
GO; GO:0006945; P:virian atrachment, binding of host cell sur. . .; IEA.
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SEQUENCE 1255 AA; 139124 MW; 1C49ACA2CFD38FC0 CRC64;
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Best Local Similarity 100.
Matches 17; Conservative
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